

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

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1 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCTG
51 CGCCAGGATG GAGTTCGTGA AATGCCTTGG CCACCCGAA GAGTCTACA
101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
151 GACCAGGACT CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA
201 TCAGACCAGT CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA
251 TGCGCAAGCG AGTGTGCATA TTTTATCTGG TTCTCCGAGC TCTGGACACA
301 CTGGAAGATG ACATGACCAT CAGTGTGGA AAGAAGGTCC CGCTGTTACA
351 CAACTTTCAC TCTTTCCTTT ACCAACCAGA CTGGCGGTTT ATGGAGAGCA
401 AGGAGAAGGA TCGCCAGGTG CTGGAGGACT TCCCAACGTA CTGCCACTAT
451 GTTGCTGGGC TGGTCGGAAT TGGCCTTTCC CGTCTTTTCT CAGCCTCAGA
501 GTTTGAAGAC CCCTTAGTTG GTGAAGATAC AGAACGTGCC AACTCTATGG
551 GCCTGTTTCT CGAGAAAACA AACATCATCC GTGACTATCT GGAAGACCAG
601 CAAGGAAGAA GAGAGTTCTG GCCTCAAGAG GTTTGGAGCA GGTATGTTAA
651 GAAGTTAGGG GATTTTGCTA AGCCGGAGAA TATTGACTTG GCCGTGCAGT
701 GCCTGAATGA ACTTATAACC AATGCACTGC ACCACATCCC AGATGTCATC
751 ACCTACCTTT CGAGACTCAG AAACCAGAGT GTGTTTAACT TCTGTGCTAT
801 TCCACAGGTG ATGGCCATTG CCACTTTGGC TGCCTGTTAT AATAACCAGC
851 AGGTGTTCAA AGGGGCAGTG AAGATTCGGA AAGGGCAAGC AGTGACCCTC
901 ATGATGGATG CCACCAATAT GCCAGCTGTC AAAGCCATCA TATATCAGTA
951 TATGGAAGAG ATTTATCATA GAATCCCCGA CTCAGACCCA TCTTCTAGCA
1001 AAACAAGGCA GATCATCTCC ACCATCCGGA CGCAGAATCT TCCCAACTGT
1051 CAGCTGATTT CCCGAAGCCA CTACTCCCC ATCTACCTGT CGTTTGTGTCAT
1101 GCTTTTGGCT GCCCTGAGCT GGCAGTACCT GACCACTCTC TCCCAGGTAA
1151 CAGAAGACTA TGTTCAAGCT GGAGAACACT GATCCCAAAT TTGTCCATAG
1201 CTGAAGTCCA CCATAAAGTG GATTTACTTT TTTTCTTTAA GGATGGATGT
1251 TGTGTTCTCT TTATTTTCTT CCTACTACTT TAATCCCTAA AAGAACGCTG
1301 TGTGGCTGGG ACCTTTAGGA AAGTGAAATG CAGGTGAGAA GAACCTAAAC
1351 ATGAAAGGAA AGGGTGCCCT ATCCCAGCAA CCTGTCCTTG TGGGTGATGA
1401 TCACTGTGCT GCTTGCGGCT CATGGCAGAG CATTCACTGC CACGGTTTAG
1451 GTGAAGTCGC TGCATATGTG ACTGTCATGA GATCCTACTT AGTATGATCC
1501 TGGCTAGAAT GATAATTAAA AGTATTTAAT TTGAAAAAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1601 AAAAAA (SEQ ID NO:1)

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FEATURES:

5'UTR: 1-57
Start Codon: 58
Stop Codon: 1180
3'UTR: 1183

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 108000024649260 /altid=gi 12734163 /def=ref XP_005134.2 fa...	770	0.0
CRA 18000004925908 /altid=gi 4758350 /def=ref NP_004453.1 farn...	743	0.0
CRA 18000004929946 /altid=gi 2135096 /def=pir I38245 farnesyl-...	741	0.0
CRA 18000004993865 /altid=gi 2136196 /def=pir I52090 squalene ...	740	0.0
CRA 18000004932414 /altid=gi 6753838 /def=ref NP_034321.1 farn...	671	0.0
CRA 18000004937535 /altid=gi 9506591 /def=ref NP_062111.1 farn...	654	0.0
CRA 1000682330885 /altid=gi 6002565 /def=gb AAF00038.1 (AF0903...	582	e-165
CRA 335001098694081 /altid=gi 11514495 /def=pdb 1EZFA Chain A,...	579	e-164
CRA 18000005103884 /altid=gi 2463565 /def=dbj BAA22557.1 (AB00...	282	1e-74
CRA 18000005103885 /altid=gi 7434086 /def=pir T00489 farnesyl-...	280	4e-74

FIGURE 1A

BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960...	1441	0.0
gi 12945082 /dataset=dbest /taxon=960...	1370	0.0
gi 12921315 /dataset=dbest /taxon=960...	1346	0.0
gi 11642571 /dataset=dbest /taxon=96...	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606...	1281	0.0
gi 13040072 /dataset=dbest /taxon=960...	1233	0.0
gi 12944143 /dataset=dbest /taxon=960...	1055	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12926380 placenta
gi|12945082 T cells from T cell leukemia
gi|12921315 Fetal brain
gi|11642571pancreas
gi|9141948 Burkitt lymphoma
gi|13040072 bladder

From tissue screening panels:

Whole liver

FIGURE 1B

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMKP MDQDSLSSSL KTCYKYLNQ
51 SRSFAAVIQA LDGEMRNAVC IFYLVLRALD TLEDDMTISV EKKVPLLHNF
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE
151 DPLVGEDTER ANSMGLFLQK TNIIIRDYLED QQGGREFWPQ EVWSRYVKKL
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPQ
251 VMAIATLAAC YNNQOVFKGA VKIRKGQAVT LMMDATNMPA VKAIYQYME
301 EIYHRIPDS PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 2

1 48-51 NQTS
2 239-242 NQSV

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 5

1 39-41 SLK
2 50-52 TSR
3 158-160 TER
4 313-315 SSK
5 322-324 TIR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 3

1 81-84 TLED
2 145-148 SASE
3 147-150 SEFE

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

1 137-142 GIGLSR
2 276-281 GQAVTL

[5] PDOC00009 PS00009 AMIDATION
Amidation site

22-25 GGKR

[6] PDOC00802 PS01044 SQUALEN_PHYTOEN_SYN_1
Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL

[7] PDOC00802 PS01045 SQUALEN_PHYTOEN_SYN_2
Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQQGGREFWP

FIGURE 2A

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	125	145	0.834	Putative
2	241	261	1.467	Certain
3	339	359	1.716	Certain

FIGURE 2B

BLAST Alignment to Top Hit:

```
>CRA|18000004925908 /altid=gi|4758350 /def=ref|NP_004453.1|
    farnesyl-diphosphate farnesyltransferase 1;
    Farnesyl-diphosphate farnesyltransferase 1 (squalene
    synthase); Squalene synthase [Homo sapiens] /org=Homo
    sapiens /taxon=9606 /dataset=nraa /length=417
    Length = 417

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA
Sbjct: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60

Query: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121  VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 121  VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138   IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
          IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 181   IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198   KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257
          KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL
Sbjct: 241   KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300

Query: 258   AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR 317
          AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR
Sbjct: 301   AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR 360

Query: 318   QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 374
          QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH
Sbjct: 361   QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 417 (SEQ
ID NO:4)
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>CRA|108000024649260 /altid=gi|12734163 /def=ref|XP_005134.2|
    farnesyl-diphosphate farnesyltransferase 1 [Homo
    sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
    /length=431
    Length = 431

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA
Sbjct: 15   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 74

Query: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 75   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 134

Query: 121  VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 135  VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194
```

FIGURE 2C

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 195 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 254

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 257
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL
Sbjct: 255 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 314

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR
Sbjct: 315 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 374

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 374
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH
Sbjct: 375 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 431 (SEQ
ID NO:5)

>CRA|18000004929946 /altid=gi|2135096 /def=pir||I38245
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21),
hepatic - human /org=human /taxon=9606 /dataset=nraa
/length=417
Length = 417

Score = 741 bits (1893), Expect = 0.0
Identities = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137
VLEDFPT YCHYVAGLVG
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 257
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 300

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR
Sbjct: 301 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 360

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 374
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH
Sbjct: 361 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 417 (SEQ
ID NO:6)

FIGURE 2D

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00494	1/2	47	126 ..	1	88 [.	124.6	1.1e-33
PF00494	2/2	127	291 ..	146	317 .]	301.1	1.3e-86

FIGURE 2E

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1  TATTTATTCC TAATTAAATG GGGAGGAAAG TCTTTGAAGA GGAACCTCTA
51  CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTTT
101 TGGGGTTCCC TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG
151 GACTTAGGAT TTTTAGTTTA CAGTAGTAGG GGAAACACTC TGTAATCTAA
201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC
251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG
301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA
351 GTATCTGGGG GATAGTGCAG GAATAGTGAA CAGCTAGACA AAAAGTCCTA
401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG
451 GGTGGAAGGC TGCAGCCTCT CAGGATCCCT ATAGGTGCTT TGGCTTTTGT
501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTTCC
551 TGTTTGTTTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA
601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT
651 TCTCGTGCCT CAGCCTCCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA
701 TGCCTGGCTA ATTTTGTAT TTTTAGTAGA GACGCAGTTT CAGCATGTTG
751 GCCAGGCTGG TCTTGAACCT CAGACCTCAG GTGATCCGCC CGCCTTGGCC
801 TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCCTC GGCTAGACCT
851 GACAGGTTTT AAAAGGATTA CTGGTTGCTG TGTTAAACA GACTGCAGGA
901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTTT TTTTGGAGAC GTAGTCTTGC
951 TCTGTTGGCC TGGCTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC
1001 TCCGCTTCCC GGGTTCAAGT GATTCTCCTG CCTCAGCCTC CGGAGTAGTT
1051 GGGACTACAG GCGCCACCA CCACACTCGG CTTTTTTGTA TTTTATAGTAG
1101 AGACGGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT
1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTT GCGATTACAG GCGTGAGCCA
1201 CCACGCCTGG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA
1251 TGAGAGAAAT TCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAGCTCC
1301 TTTTCTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGCGAGC
1351 TGAAGCTCCA GGAGTGTGTG GGGCTCCCTG GGGCTGGATG GCGGTGGCGG
1401 GCAGGCGAGC TGGGCTGTGC TCGGCTGTGT TACAGTAAAG ACGCCCAGCT
1451 TGGCGCTGGC CCGGCCTTTT CACGGTTTTA GGCTCTACAG AGAGCGGCTG
1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGAGCA CGTGGGCGAC
1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACTGCTCT CCCGACTGCG
1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG
1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG
1701 CCCGGCTCCA TCAGGGCACC AATCCCGCTC GTCGGCCTCT TTCTCGGCCT
1751 CCAATGAGCT TCTAGGGTGT TATCACGCCA GTCTCCTTCC GCGACTGATT
1801 GGCCGGGGTC TTCTAGTGTG GAGCGGCCCT GGCCAATCAG GCGCCCGTCA
1851 GCCCACCCCA CGAGGCCGCA GCTAGCCCCG CTGGCGGCCG AGGCCGGTTG
1901 AAGTGGGCGG AGCGGCGGGC GGGGCGTCGC CGTACTAGG C TGCCCCCTG
1951 TCCGGCCAGC CCTCGAAGC ACCTACTCCA CAGGTCCAGC CGGCCGGTGA
2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCTG
2051 CGCCAGGATG GAGTTCGTGA AATGCCTTGG CCACCCCGAA GAGTTCTACA
2101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
2151 GACCAGGTGG GCCGAGCCTC CCTGCTTGCC CGGGGCGGGG AAGGAGCTCG
2201 CTGGGCGGGC CTCAGGGCCT GAGCGGCCGG GCCCGGATCT GGGGCAAGGG
2251 GCGGCGCGAG CAGGGCCGAC GCCTGGGTGT TCCCGTCCCC CTTTCCTCGA
2301 GCCTTCCCCC TGTAGGGCCC GGGTGGACGC GGCCGTCTCG GCTGACCTGT
2351 CCCTGCCCCC GCAAGCCGCC CTGGGCATGA GCGACTTTTG CGTGGTTCCT
2401 GGTGGTTGCG CTCCTCGTTT CGTCCCCTCC GTGAGCATCG GCGCTTACCG
2451 GTATTTTAAC CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC
2501 GGGAGAGGAC GAGTGAGTTT TTTGGTAAGC GGAATGAACT ATGCAGATAA
2551 CATCATGA AGGCCGTTTC TGGAATGAAG TCTGACTCCT CCAGTTTCAC
2601 CACCTCTTCC GAGCTCTCC CCGCCTTGCT GCCTTCCATC GCTTCATCCT
2651 CGGTGCTTCC TGAGTTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT
2701 GAGTTATCTA ACGTCTATGG ATTAGCTAGG TGGTTGGTGG AAGGTCAGAA
2751 CTTGGTTTTA CTTAGATTTT TATCTGCCTC ATGCCTGTAC TATTGTTTAA
2801 ATGAATGCAT AGGAGGTGTT TTTATTCCAA CAAGAAATT ATTCGTACGC
2851 GATTATTGAA TGAATAGACA AATTCAAGCA AGTTCTTCTG GTCTGGACCA
2901 GCCTGGCTGA TTTCTGTAAC TTTTGGGC CAACAGGACA GTAGCAAATG
2951 TGA CTAGGC CGAGGCTTGA TAGGTGCCTG AACATCGAG TCTTTCTTTC
3001 AGTGTCCATG TGCTTCAGTA AACACACTAG AAAATAAATT TCTGGTTTTT
3051 GTCCCCAGTA GACTACACCC TCATTTGGTG TTATTTTCA CGTGCTATCT
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FIGURE 2A


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3101 TTAATACAGG TACATCCTTC AGTCTATTTC TAGAACATTC AGTTTCTCTC
3151 ATCTTTTCTT TGCCGGTGCT ACATTATTTC AATTATTTTC CTACAGAATA
3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTATATAT TAGATATAGC
3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT
3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT
3351 TTATAAAACT TACTTTTTAG TGGAAGAGAG ACAATTTAAA AAAGCGAATG
3401 TACAGTTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG
3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCATTCCT
3501 CTATGTCTCT TTCCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT
3551 TGGTTTCCTG TTGGGAGGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA
3601 AAGACTTCAC AGTATACGTG TTTTGTACAT TTTGAGTTTT TTTAAAAGCG
3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT
3701 AGTTGTAGTC TTTCTGGGCA GTTTTTACAT CCCCATGAGC CGTTAAAAAA
3751 ATACCTGAAC CTTTAATTAG GGGAAATAAA TTGGAAAAAT ACATTCCCTT
3801 TCACTTAACA TTATCTTAGT TTCTCTTTTT TTTTTTTTTT TTTTTTGAGA
3851 TGGAGTCTTG CTCTGTTACC CAGGCTGGAG TGCAGTGGTG GCGGGACCTC
3901 AGCTAGATGC AGCCTCCGCC TCCTGGGTTC AAGCAATTCT CCTGCCTCAG
3951 CCTGCTGAGT AGCTGGGATT ACAGGCACCT GCCACTACGC CCGGCTGATT
4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTTC ACCATGTTGG CGAGGCTGGT
4051 TTTGAACTCT TGACTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC
4101 TAGGATTACA GGCGTGAGCC ACTGCACCCG GCCTTTTTTT TTTTTTTTTT
4151 GAGGGGGGGG TCTCACTCCA TCGTCCAGGC TAGAATGCTG TGGCCTGAAC
4201 ATGACTCACT CCAGTTTTGA CTTCTTGGC TGAAGCCATC CTCCCACCTC
4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA
4301 TGGCTAATTT TTAAATTTTT TTGTAGACAC AATGTCTCGC TGCATTGCCC
4351 AGGCTGGTCT TGAACCTCTG AGCTCAAGCG ATTTTCCCAC CTCAGCCTTC
4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCAACC AGTTTCTCTC
4451 TGCAAAC TAGGAAAAATT TACGCTTAGC AGATATTGAG GGCTGATTAT
4501 TTCTATCACA GAAGCATTTG GCTATAGAAT TTCAGGGTTT AGTAAACTTG
4551 ATTTACACTG AATTTTTTAGG TGCATATCAG TAAATCTACG GGCATATGCC
4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC
4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT
4701 TATTTAGACT AATATCTTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA
4751 TTAAGTTAGG TGAACAACTT TGGTAACCTA ACCTCTGAAC CACAGTTACT
4801 TCATCTGTAA AATAGGGATG TATGTATGGT AACGATTTTT TAACCACAAC
4851 TTCCCAACTC TAAGATGGTC TGAAAAGAAT TTTTGTAGTG TTTGGCTCAG
4901 AATCACTTGG CAGCAAAACC TGACTTGAAG TTGAGGCTTC ATTCATCCCA
4951 CTTAGTATAT TCAAATGTTT TGCTAAAGAA ATAATTATGA GGTGCTACTT
5001 CACACTGACT AGGGTTGTAT ATGCATTTTA TTGCCTATTT TCTAAAACAC
5051 TAAAAATGCT AAATTTCTGCC CCAGGTCTTG CCACAGATGT TTCAGTGGAC
5101 TATGGGCCTG TGAGACCTTA AAGGGTTGAT TGAGTAAGGA TCACAGGTGA
5151 TGTCCGCATT GTGCTTGCCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA
5201 TCAATCTGAT TATGTAAATT TATGTAAATT CAGTTCTCAA GTTTGTGGTT
5251 TTTTTCCTCT CCTGGAGAAA TCTATTCTAT TTTAAAGTGA GGAAGGCTCC
5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTTAC TTGTGGAACT TTCAGCCTGA
5351 GGCTGGAGCC CCTTCTTGGG AGTCTGGTCT TGTCGTCTTC CTGACCACCC
5401 CCACACCCTT CCTCTAAATT CCCTCCATCC CTGTTTTTCT CCCGCTTGCG
5451 AGCTTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCCAAGAG
5501 GGACAGGCAC CAGTAGCCTG AGCTTGCTTT CTCCCCTGGC TCATGGGAAT
5551 CAAGCAGTAG AAATTTTTAG TGAGTGTGTG TTTCCATAGT ATGCTTACTA
5601 GTTGTGTCTT CCTGTTTTGT TCTTGGTGAT TTGAAGAAAC CTGTTTACAA
5651 GGTAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC
5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT
5751 GTATGGAAAG GAGGGTAGT GTTCTTGAAG AGTGTGGGG TTTAAATCTA
5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCCTGGCTTA ACATCACCCC
5851 GAACTGTGTA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAAACA
5901 CTTCTGCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG
5951 AGCTCAGTCC AGAGCGGGTA TTCTGTTTCT TTCACTCTGA AATCCTGCCT
6001 CTCGATATTT TGAGAAGGAA GGAGTTGGTG AATTGTTTTA AAATCCTCGA
6051 TGAATGTCTT CATTTATTCA TGACACCCT TCTGAATATA TTTATGTGCC
6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTTA
6151 CTAATATTTT TTATGGCAAT AAAATGACTT TTTCAGGATT ATGTGATTTA

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FIGURE 2B

6201 AAAGATTGAC CCTTTTGGCA AAATACGTAT TCATGATAGG AAATATATAC
6251 AACATAGTTC ACTTAAACCT CCCACCAGAG CCCAGGGTTC ACTGTTACCA
6301 TTCTGAAGTG ACTGGAATTT CCTAGAAGTG GATATGCCAT ATTTTTTTAA
6351 CCACTCCTAT TGGATATTTG TTTTTTATTT TTTTGAGATG GGGTCCCCT
6401 CTGCAGTGTA CAATATCATA GTTCACTGTA ACGTGTATCT CTTGGGCTCA
6451 AGCGATCCTC CCCACCTCAG CCTCCCTGAG TAGCTAGTCT TCAGTAGCTA
6501 GACTATAGGT GGGCGCCACC ACAGCTGGCT TTTTAAAAAA TTTTTTATGA
6551 ACACGAGGTC TCACTATGTT GCCCAGGCTG CCCTCAAACCT CCTGGGCTCA
6601 AGTGATTCTC CCACCTTGGC CTTCCGAAGT GCAGGGATTA TAGGCGTGCG
6651 CCACTGCACC CGGCCCTGTT GGATAAATGA TTCCAGTCTC TCCCAAAAAG
6701 AACTGTTGTA AGACTGTGGG GTGAGGGGAG GGAAGGGACA AATAGGAACC
6751 CGCCGTATTT TCCACTCCCT GTGGGCCTAA AACTGCTCTA AAAAATAGTC
6801 CATGAAAAAA TACATAGTAC AAACAGCAAC TCTTTCTGAT ATGCTTGCA
6851 TTAAAAATCAG GCTTTTTCTC CTTTTTGGAA AAACACAGTC CTTGTTTGCT
6901 TTAGGGAAGA GTAAAGGTCA GTGCGCTGCA TTGCATTAAT TTCGAAGGGA
6951 AAGATGAGAA GACATCTTGA AAGGAATGGC TGGCTTTCTA GAGAATAGTA
7001 GAGGCTTAAT AGGTGTCATA GAAAAACCAG GGTTGGACAG TGGTAGTAAA
7051 ACGGCAAAAC AGATTTTATT CAGAAAAACT ACTGCAGTAA GAGGAGAGAG
7101 ACCTCGGTAC AGAAGTGCCT CACTGCGAAT ACAAAGAAAA GTAGGAATTG
7151 ATGGCGGGGG AGCCGGATGT CAGTGGATGG AAAATTATTA CGAGGAAACA
7201 CAGGGGTGTG CATCTTGCT GAAGGCAGGC CAGAGTTATC AGACATCACC
7251 TGAGGGATGG AGGGGATGT GGAACCTAAT CGGCTGTCTA GGGTGATCAG
7301 ATACTGAAGT TGGGGGATTC TGGTCAAATC AATTTAGCAG GATTCTTGGT
7351 AAAACTGGGC GATGCAAAGA CAGATGCGTT GAGTACAAAG TCCAGGCTTT
7401 ATTGGGAAGA GGATTTACAG GGAGCCCAG TAGAGTTTGG TCTAGGGAGA
7451 CTCTGTCACT GGGAGGACGA GCGAGCCGCT CGGAAGTGCG CTGGGTCTC
7501 TTAGCGGCCA GTGGGTTCTG GTGAGAAGGG CAACAGCGGG AGGAGGCGCC
7551 GGTGCGGAGC GGGAGGCCGG GGGCGGGGCT GCGGGGCTGC GGGGCGGGCC
7601 CGTTGTGGGT CGGCCAGCG CGTATTCGAG TAGAGGGCGA GCGCGTCCCG
7651 CCTCTCGTCG GCGCCTTCCC AGATCTGCTT GAGTCTATGG AGGAAAAACT
7701 CCGCGGGGTC CGCGATTCCC ATGGCCGCG CCGCCTGCGG CACCAAGGCC
7751 ATGGCCCTCT TCAAGCGCAC CTTGGTGTG AGTCCCGCCG CGGCGCCCAG
7801 GGGCCCGGGC CAGGACCCG CCCC CGGGG CTGCTGCTTG CCTCCTGCCG
7851 CCTGGCCCTG CAAGGACTGG CCTCGGGGAG AGGGCGGCAG GCTGTGGAGC
7901 CGCCTGCCCC AGTCCAGTC CCACTCCAC TCCCACTCCC ACTCCCACTC
7951 CTGCTCCTCG ACGTCTCCA CCGCCGTGTG TGTGTCTGC CCGCAGGACT
8001 CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA TCAGACCAGT
8051 CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGAAA TGCGGTGAGT
8101 GATGGAGGCA GCGCCTCTGG CTTGGAGGAA AGCTTGTCGG GGACTTTTGA
8151 GTGTGTTGGA AGCTACCTTT TGATATAGCG CTCAGCGTTG CAGCCTCGTT
8201 GCTGTGGCTT ATCCAGAACA TAGCCCGGCC CTACGTGTTT ACTTTAGAAA
8251 GCCCTTCCAG GCTCTTTGCC ATCTAGTAGA GTCCCTGCGG GCCCAGCCTT
8301 TCAGAGAAGG GGGGGGAGGG GGTGATGTTT ATTAACTTT TTTAGTCTTG
8351 GCAGCTGAAC CTGCCTGTGA GCAGGTCGTG TATTTCTCGG CTTCCCTTAT
8401 CCAACTTTGC ATTTCTATTT CTAGCATATT GGGTTGATTC TTTTGAAGCT
8451 CCCTCTGTGC ACATTACACC CATGAACCTA GACCAGTTGC CTTTATGTAT
8501 GATCGTATTT ATACTGAGAA GTTACTGTGT TTTTGTACTT TCTTTTCTAT
8551 TTGCTACATA TTAGTTCGGT CTAAACGTTT GGTCTTCTGG TCTCCATAGT
8601 TCTACATTGG TTAATGCAA CTCACCTCTG GGAGTAGTGG TGACATTCAA
8651 CTAGTAGGCT TTTTAATAAA CTACAGAAGT TCATTACTCT CATGTAAGGA
8701 AGGAAAACTA ATGTAACCTT CGTTAAGTAT GAAAAGCGTT GGATATCCTT
8751 ATAGTTCTTT AGAGTTAAGG GTGAGATGGG TTTAGAAAGT GGCCAGGCAC
8801 AAGTTATTTT AAAATAAAAA ATCTTTGGCT GTTTGTTCCA ATATATTAAT
8851 AGTTTTCCCT TTTTACAGC AACGCAGTGT GCATATTTTA TCTGGTTCTC
8901 CGAGCTCTGG ACACACTGGA AGATGACATG ACCATCAGTG TGGAAAAGAA
8951 GGTCCCGCTG TTACACAAC TTTACTCTTT CCTTTACCAA CCAGACTGGC
9001 GGTTCATGGA GAGCAAGGAG AAGGATCGCC AGGTGCTGGA GGACTTCCCA
9051 ACGGTGAGTG GGGTTACGCA TCTTGTCTAC GGACTGTTGT GTTCATAATT
9101 GCTAACGTGG TTGTCCGTA GCCTCCATAC ATGTGGAGAA AGGTTAAATA
9151 AGCATTCTGA GGCAGCATA ATGTGAGGGT TAAAAACTCC GGTAGCCAAG
9201 ACTCTGAAGC CAGGCTGCCT GGGTTGGAAT CTCAAATCTC CCACTTACTA
9251 AACTGTTGGT TACTTACAAA GACTCTCTGT GCCTCAGTTT CTTTCTCTGT

FIGURE 2C

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9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA
9351 GAATTAACGT AGGTAATGCT CTTAGAATGT TAGCTACTGC TGTATTATATC
9401 AGTATTGGAA GTCCAGTGTT TCTTCCTGTG GGAAGACGCA GTCAAATTTT
9451 AGTGTGTGTA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT
9501 GATGCAGCCT ACCTGTAACA CTGCTGGCCT CTTGACTACC CGGAGCCTGG
9551 TAGCATGGGA CTGCTGCTCA CGATGGGCAG CAGCCTGGCA TGGGGGCGGT
9601 GTCTGTTGGC AGCTAGGGCG AGCCTCTGCC ACTTCACCTG TGATCCTGGG
9651 CAAGTTCCTT ATCTGCTTTG TGTCTCCGTC TCCTCGTTTG TAAAGTTAGA
9701 GCTGAGAGGA TTAATTTTCG ACATATAAAG TACTTAGTGC CTGGTACAGG
9751 GTAAGTATTC TGTAAGTATT AGCTATTTGG TCTATTTTGT TGGAGTAAAG
9801 TGGGTTATAG TTAATAATCCT AAGATTTTFA AAGTCCCTCA AGTTCACGTG
9851 GACATCTGCC TAGGTCCCTAC TATCCTAGAA TTCGCATGTC TTATCACACA
9901 AATAATCTGAT TCTTCCATAT CTTATAAATA AAGGTTTGAT TTAGCAAAGT
9951 CACATGTTGT GTAATAGCTC GAAGAAGCCC TTTTGTGCCA CAGTTGCCAG
10001 AGCTTTTGGG GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC
10051 TGAGTTGGGA GGGAGCTAAG TGGACAGAGA GTCCTCCACC CAAACAAAAG
10101 AATCTTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAA AAAAAAAAAA
10151 AAAAAAAAAA GGAATGTTTG GGGAAGACTC TTGCGGTGCA AAGGCTGTTT
10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAAT ATAGTACAAC
10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAAATCGA GTTTATACAG
10301 TACAATTCAA GAGAAGAAAG AAAATTTATG ACGACTAGCT GGGTGAGAAT
10351 TAGAACTGTA ACCCTGGGAA GGTCTTGGTG ATTTGACTCT CACAGGACAC
10401 CTGATGACCA GAGGATGGGT TTCCTTTGAT GGGAAATCTG TGGCGATTCA
10451 TTGATGGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCCAT
10501 TTATAATGGA AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT
10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA
10601 TAATAATTAA AAAATTTCTG GGGCATGGGA TAAATGTGTT AGGTATTGCT
10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG
10701 TGTGAATGCT AACATAATTT TGGGGAATAT CGCCGTCAGA TTTCCAGATG
10751 ATATTCCAAC ATGTTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT
10801 GTTCCAGTGG AAAAATAATG CTTAGTTCCTG GAAGGTTTCA GATGTGAACA
10851 CTGAATCAT CGTTTTCTTT TTTGGGTAGT AGAGTTAGAG ATTCCATCCT
10901 CTTGAAAGCA CAGTTGCCCC GGGAAGAGTA AAAGGGAGCA GAAGGCGTAA
10951 GCCAGGCACG GCTGTTTTCA CTGTTGTTCA CCTTTTGTAT CCTTACGAAT
11001 ATGAAGATGT ACTAAGTTGT GTGTTTTGCG TGCATATATA ATTTTAAGCT
11051 ACTTGAGTTG TAGGTCCCTC CAGTCTGTGA TTCAGTTTGA GATGGGACTG
11101 TATGGGAATT AACAGTGCCT TGTCTTCTTA AGCAGTGATT TGTGTATGTG
11151 CTGATATAGC TCAGTATGTC TTTGAAACCA GTTGTCTGGG GCTAGGCCTG
11201 CAATCAGCTT TTGGCTAAGA GGTCCCAGGA TGGAACAAGT AGTGTGAAAG
11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGGCAA
11301 GTGAAACTCC TCACTTCAGA GTGCCCCATT CTAGGCCCCC TCACTCCCAA
11351 AGGGGTGAGG GATCACTGGG GCCATGGGAA TGTGCTTGTT CAGCTCTCGT
11401 GGGCTCTCCT TCTGTACCAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA
11451 ATCCCTGAGC CCACGTCTGC GTCCGCACAG TCTATTTTCT AAGGTCAGTC
11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGAATGTGCC CTTGGGCCTG
11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTGGATGG ATCCTGGCAC
11601 CGAGGGCTGG GATATCCTCT CAAATGAATG TGAGGTGCCT CCCAGTGCTG
11651 GAGAGAGCGG GATTCAAGAA GCAGTGGAAG GGAAGAGCCT GGGATATGGG
11701 GATCAGCTGT CTGTGCCCTG CTGCATTCTG GAATAAAACT CTGAGGGACT
11751 AAGAATTCTA AATTCAAACC TGAATCAACC AGGTTGTTAC AAAGATAAGT
11801 TTGTCAGTGC AGGAGGATAC AATATATTTT ACTTAAGTTA CTAGCTCGAT
11851 TGATCATTTT TAAATTTTTA GCTACATATA GTATGTGGG CTCCATTTGT
11901 CCTCTTATCC CAGGCCTTGC AGAATTTAGG AATAAGCCTC AATACAGTGT
11951 TCTAACCCAG TGACTTCCGC CTCGATGTAC AGTAGATTGA ACCTGATCCT
12001 TTATACTTTA GTGATCATTA GTTGATACCA GTTCAAGTCA GGCTTTCTAG
12051 AAATCTCATT GTATGTTAGG GGTTTCGATTA GAGTACAGTC ATGCATCACT
12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT
12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT
12201 AGCTACTACA GACGTAGGCT CTGTGGTACA GGCCATTGCT CCAAGGCTGC
12251 ACATCTCTAC AGGATGGTAC TGTACTGAAT ACTGTAGGCA ATTGGAGCAC
12301 AGTGGTAAGT ATTTGTGTAT TTAACATAG AAAAGGTATA GTAAAAACAG
12351 GGTGTTACAG TCTTAAGGCG CCACCATTGT ATTTCCAGTC TCCGTTGACT

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FIGURE 2D

12401	GAAACATCAT	TATACAGTAC	ATGAGCACGT	ATCTTTCTCA	CCTGGTACTA
12451	GTGGAAAGCT	AGAAGGCTTA	GAAGTCTACC	TGTAAACATA	GCTTAAGTAA
12501	TAATACAGCC	TTATTTTTTA	ATGATAATAG	CAATAATAGT	GTTCACTTAT
12551	TGAGCATTTT	ACTATGAGTT	ACTTACTAAA	TATATTTTCA	CGTTAATTTA
12601	CTCTTTGTGT	TATTTTGATCT	ATAACATCGT	TTAACAGGGA	AATTACCTAG
12651	TACATAATGT	ACTGTTATCT	ACATTTTATC	TAGATGAGGA	AACTGAGGCA
12701	CAGAGAAATT	AAGTACTTTG	CCTAGGATTA	CCCGTGAAGT	TAAGTGACAG
12751	AATCAATGAA	TCTGGAAGGT	CTGGCTTCAG	ATCTCTGTGT	CTGAGTCACT
12801	CGCATACTTT	ACTACCTCTA	AGGTTTCTAA	TCAGAGGAAT	TTGTATCTGT
12851	ATTCCCTGCT	ACTCTTACCC	TCTATGTGGG	ATTTGGCCTT	TCTCCATTAT
12901	CCCTGTGAAC	TCGCTCTGGG	ACCTTCCTTC	TTGTACTTGG	AACCATCAGA
12951	AAGTGATCTG	AGAACATAGA	AATCTACTGT	GTTGTGAAAC	AGAATTACCT
13001	GGAAGCGGAA	AAAGCCCTCC	TGGCTCAATT	CACATGTCAC	GGCTTATGGT
13051	CGTATCCGGG	GAACATATGA	AACTGGGCAC	TGAGTGCGGA	GTCAGGAAAG
13101	CCCTGTCCAT	CCTCTGGGTT	TCTGGGGAAA	ACGTGGACCC	CTTCATTGTC
13151	ACTTTCTCCT	GTATATTTTT	GTTTTTACTT	TTAGAACTGT	ACAATTACGT
13201	AATAAATAAT	AAAAAGTCGT	TGGAAGGATA	GGTGAAGTTC	AGAAGTAAA
13251	GTGTTTTGGA	GGAGTCTAAG	CTCCTTCCCA	CCCTCATTGA	CCTTTCCTCT
13301	CTAATAAATA	GAACTGGTCT	AACCAAGGAT	CTGTGGAATG	AGCAGAGTCC
13351	AACGGAGATT	CAGGGATTCT	AATAACCTCT	TGTAGAATCA	CTGGTTTGTT
13401	TCAGCCACAA	GAGGAATTA	CCTTTTGACA	TTGGCTTGAA	CAGCTGTTGT
13451	GCAAAGAAAA	ACTTTTTGGA	AAGTTCTGGA	AGTACCAGAT	TGATTTTATA
13501	GGTTTTTTTT	TTTTTTTTTG	GAGGGACATG	GGGGTATTGA	CAGTTGATGT
13551	TAATCAGAAA	TCCTAAATTA	TGTGTATTCC	TGGTATGTG	CAATCAGCCG
13601	GCCACCTGGT	TTTCTCTGG	GCTCTTAATT	TTAGGTGTAT	TCCGAGGAAG
13651	TTTTTCTAAC	TTTTCTGTAA	ACACAGACCA	GGTATATTGC	ATACTTTCAA
13701	TGTTTAACCA	AATCTCTTCA	CTGTTTGCAG	TATTATCTGT	AGGCTCTCAT
13751	GTTTTAAGAC	TTCCCCATGG	TGTTTTTGTA	TTGTATTTTG	CTAACCTATA
13801	AACAATTCTT	TGAACTTAAA	ACAAGATATT	TGGGCAGTAA	CAATAAATTT
13851	TAAAAACATC	AATTCAACTT	TTTTACATTA	GGGCTTGGAC	TATGGAAAAA
13901	GTATTGGGCA	GCATGCCTCA	TACTGAGTTG	TTTAATGAAT	TTAAAAGTAT
13951	AGCCNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 2E

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

15501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17551	NNNNNNNGGT	GGAGAGTTCT	GTAGATGTCT	GTTAGGTCTG	CTTGGTCCAG
17601	AGCTGAGTTC	AAGTCCTGGA	TATCCTTGTT	AACCTTTTGT	CTTGTTGATC
17651	TATCTAATAT	TGACAGTGGG	ATGTTAGACT	CGCACACAAT	AATAATGAGA
17701	GACTTTAAGT	CTTTTCTAG	GTCTCTAAGG	ACTTGCTTTA	TGAATCTGGG
17751	TGCTCCTGTA	TTGGGTACAT	ATATGTTTAA	GATAGTTAGC	TCTTCTTGTT
17801	GAATTGATCC	CTTTACCATT	ATGTAGTGGC	CTTCTTTGTC	TCTTTTGATC
17851	TTAGTTGGTT	TAAAGTCTGT	TTTATTAGAG	ACTAGGATTG	CATTCCCTGC
17901	TTTTTTTTTT	CGCTTGGTAG	ATCTTCCTCC	AGCTGTTTAT	TTTGAGCCTA
17951	TGTGCATCTC	TGCACGTGAG	ACGGGTCTCC	TGAATACAGC	ACAGTGACGG
18001	GCCTTGACTG	TTTATCCAAT	TGCCAGTCT	GCGTCTTTTA	ACTGGGGCAT
18051	TTAGCCCACT	TATATTTAAG	GTTAATATTG	TTATGTTTGA	ATTTGATCTG
18101	TCATTATGAT	GTTTGCTGGT	TATTTTGCCC	ATTAATTGAT	GCAGTTTCTT
18151	CCTAGCCTCG	ATGGTCTTTA	CAATTTGGCA	TGTTTTTGCA	GTGGCTGGTA
18201	CCAGTTGTTT	CTTTCCATT	TACTGCTTC	CTTCAGGAGC	TCTTTTAGGG
18251	CAGGCCTGGT	GGTGACAAAA	TCTCTGAGCA	TTTGCTTGTC	TGTGAAGGAT
18301	TTTATTTCTC	CTTCACTTGT	GAAACTTAGT	TTGGCTGGTT	ATGAGATTCT
18351	GGGTTGAAAA	ATGCTGAATA	TTGGCCCCCA	CTCTCTTCTG	
18401	GCTTGTAGGG	TTTCTGCTGA	GAGATCTGCT	GTTAGTCTGA	TGGGCTTCCC
18451	TTTGTGGGTA	ACCCGACCTT	TCTCTCTGGC	AGCCCTTAAC	ATTTTTTCCT
18501	TCATTCAAC	GTTGGTGAAT	CTGACAATTA	CGTATCTTGG	GATTGCGCTT
18551	CTCGAGGAAT	GTCTTTGTGG	TGTTCTCTGT	ATTCCTGAA	TTTGAATGTT

FIGURE 2F

18601	GACCTGCCTT	GCTAGGTTGG	GGAAGTTCTC	CTGGATAATA	TACTGAAGAG
18651	TGTTTTGTAA	CTTGGTTCCA	TTCTGTCTAT	CACTTTCAGG	TACAACAATC
18701	ATAGCATTGG	TCTTTTCACA	TAGTCGCATA	TTTATTGAAG	CCTTTGTTCA
18751	TTTCTTTTCA	TTCTTTTTTC	TCTAATCTTG	TCTTCTTGCT	TTATTTCATT
18801	AATTTGATCT	TCGATCACTG	ATATCCTTTC	TTCTGCTTGA	TCGAATCGGC
18851	TATTGAAGCT	TGTTTATGCT	TTGTGAAATT	CTTGTAATTT	GGTTTTTCAGC
18901	TCCATCAGGT	CATTTAAGCT	CTTCTCTACA	CTGGTTATTC	TAGTTAGCCA
18951	TTTGTCCAAC	CTTTTCTCAA	GGTTTTTAAGT	TTCTTGCGA	TGGGTCAGAA
19001	CGTGCTGCTT	TAGCTTGGAG	AAGTTTGTTA	TTACCAACCT	TCTGAAGCCT
19051	ACTTCTGTCA	ACTCGTTAAA	CTCATTGTCC	ATCCAGTTT	GTTCTTTTGC
19101	TGGTGAGGAG	TTACGTTCCCT	TTGGAGGAGA	AGAGGCGTTC	TGTTTTTGGGA
19151	ATTTTCAGCC	TTTCTGCTGT	GGTTTCTCCC	CATCTTTGTG	GTTTTATCTA
19201	CCTTTGGTCT	TGCTTTTGG	TGACGTACAG	ATGGGTTTGG	GTGTGGGTGT
19251	CCTTTTGTGT	GATATTGATC	CTATTCTTTT	GTTTGTTAGT	TTTCTTCTA
19301	ACAGAGGCC	GTCAGCTGCA	GGTCTGTTGG	AGTTGCTGGA	GGTCCACTCT
19351	AGACCTGT	TACCTGGGTA	TCACCAGTGG	AGGCTGCAGA	ACAGCAAATA
19401	TCGCGGCCTG	ATCCTTCCTC	TGGAAGCTTC	GTCCAAGAAG	GACACCCACC
19451	TATATGAGGT	GCTGTGCGGC	CCCTACTGGG	AGGTGTCTCC	TCCCAGTCAG
19501	GCTACATGGG	GCTCAGGGAC	CCACTTGAGG	AGGCAGTCTG	TCCGTTACTG
19551	GAGTTCAAAT	GCCGAGCTGG	GAGAACCCT	GCTCTCTTCA	GAGCTGTCAG
19601	GCAGGGATGT	TTAAATCTGC	AGAAGCCGTC	TGCTGCCTTT	TGTTTAGATA
19651	TGCCCTGCCC	CCAGAGATGC	AATCTAGAGA	GGCAGTAGGC	CTTGCGGTGG
19701	GCTCCACCCA	GTTCAAGCTT	CCTTGCTGCT	TTGTTTACAC	TGTGAGCATA
19751	GAAGTGCGTA	CTGAAGCCTC	AGCAATGGCG	GGGAGGCGCT	TCCCCTCACC
19801	AAGCTCCAGC	ATCCCAGCTT	GATCTCAGAC	TGCTTGGCTA	GCAGCAAGCA
19851	AGGTCCATG	GGCATGGGAC	CCCCCGAGCC	AGGCACTGGA	GGCAATCACC
19901	TGCTCTGCCA	GTTGCGAAGA	CTGGGAAAAG	CACAGTATTT	GGGCAGAGTA
19951	TACTGTTCTT	CCAGGTACAG	TCACTCACGC	CTTTCCTTGG	CTAGGAAAGG
20001	GAAATCCCCT	GACCCCTTGC	ACTTCCTGGA	TGAGGTGACG	TCCTGCCCTG
20051	CTTTGGCTCA	CCCTCCATGG	GCTGCACCCA	CTGTCCAACC	AGTGCCAATG
20101	AGATGAACCA	GGTACCTCAG	TTGGAAATGC	AGAAATCACC	CATCTTCTGC
20151	ATCGATCTTG	CTGGGAGCTG	TAGACCAGAG	CTGTTCCCTAC	TGGGGCATCT
20201	TGGAAGCAAC	TCTGGGTCTG	AGTTTCTGTT	TGTTGCCCTG	ATGTATATCC
20251	CCAGTGCCCTA	GAATGATACT	TGTTACATAG	GAAGTGCTTG	ATCCATGTTT
20301	GCACAAATGA	ATCTTTCTCA	TAATGAGGTT	TCTCTAAACA	AGCTGTTCTC
20351	CCAAAACTT	ACACCCAGCT	TTATGTTGAA	GCATCTCATT	ATACATTGGA
20401	AAGATGAAAT	GTGTAGTGAG	ACTTTGAATC	TTCTTTTGAA	TCTAGAAACA
20451	TTAGCATTTT	TAGACCATT	TATTTTAATA	TTTATGAAAT	TTATGAAATA
20501	ATAAGAAACA	TAGGGCCGGG	CTCAGTGGCT	TATGCCCTGTA	ATCCCAGCAG
20551	TTTGGGAGGC	CAGGGCTAGT	GGATCATGAG	GTCAGGAATT	TGAGACCAGC
20601	TTGGCCAACA	TGGTGAAACC	CCACTTCTAC	TAAAAATATA	AAAATTAGCT
20651	GGGCGTGGTG	GTGCATGCC	GTAATGCCAG	CTCCTGGAGA	GGCTGAGGCA
20701	GGAGAATCAT	TTGAACCTGG	GAGGCGGAGT	TTGCAGTGAG	CTGAGATCGT
20751	GCCATTGCAC	TCCAGCCTGG	GCAACATTGC	GAGACTCCAT	CTCAAAAAACA
20801	AAAACAAAAA	CAAAAAAAT	GTGTGACCTA	AATTAGGCTT	ATAGATGAAC
20851	CATTGCAGTC	ATGATTAATT	CCGCCATTGT	TTGCCTTGTG	ATCTTTGGTG
20901	CCATGTCTGT	ACATATTTCA	TGATTTCTGT	GTTTTTACGG	TTTCCATTTC
20951	AGATCTCCCT	TGAGTTTAGA	AATCTGGCTG	AGAAATACCA	AACAGTGATT
21001	GCCGACATTT	GCCGGAGAAT	GGGCATTGGG	ATGGCAGAGT	TTTTGGATAA
21051	GCATGTGACC	TCTGAACAGG	AGTGGGACAA	GGTTAGTCTC	ATAAAACAGT
21101	GTCTGTGTGT	GATGTATTAG	ACAGAGCTGG	CAGTCTCAT	AGTGAAGCTC
21151	AGAACAAGAA	AAGTTGTCCA	GTATTTTCAG	CCCCTCTGGT	TTTACAATTC
21201	ATCTGTTTAG	GTTGAATGTC	TCATCATAAA	CAGTTTATTC	CAGAGTTAAT
21251	TCCAAACCAG	CAGCTATGTA	GGATATCAGC	CAGGCTAGGA	GTAGGGTACT
21301	GGAGAGAAGT	GCTTATCTAG	ACAAAGGGAT	GTAATTGACC	ATGAAGATTA
21351	AAACTACACA	TCAAAACATA	AGGTAGGGTT	AGGAGTCTTG	CCTATTTTTC
21401	ATAGGAATGG	TGTTTGTGAG	ACTTACTCAT	CACTTCTGTG	GAAGTAAAGA
21451	CATTTTATTT	ATTTATTTTA	AAGCCAGTCA	GATTTAGCAG	GCAGAGACAT
21501	TTCCAGACATC	TAAAGTGTTG	ATGTATTTCA	TACCTTTAAC	TGTGCTTAAA
21551	TTAGGATCTC	CGAAAAGATG	CTGCTACATG	GTCACACGT	TAGTGATAGT
21601	CCAAGGTCTT	GGGCTCTTAA	ATTTTTCAAA	CCTCAAACT	TGACAGCAGT
21651	TATCTTTGGA	ACTGCTGATT	TGTGCTTCTC	AAGTTAACAG	CATACAATGA

FIGURE 2G

21701 CTGCTAGAAA TCAATTTCTG CATTTAAGGT GAAGTTAGCC GGGTACTATG
21751 GTTTACCTGT AATCTCAGCA CTTTGGGAGG CTGAGGTGGG AGGATCATT
21801 GAGCCCAGGA GTTAGACACA AGCCTAAGCA ACATAGCGAG ACCCGTCTT
21851 TCAAAAAATT AAAAAATGAG CAGGGAATTG GTGGCATGTG CCTGTGGTCC
21901 CCAGCTACTC TGGAGGCTGA GGTGTGGGAG GATTGCTTGA GCCCAAGAGT
21951 TGAAGGTTGC AGTGAGCCAT GATTGTGCCA CTGCACTCCA ACGTGGGTGA
22001 CAGAGCAAGA CACCTACTGA AAGAAAATAA AGTTGAAGTT AAAACTTCTG
22051 GCCAAGAACC AGCACTGGTT ATGATAGTAA CTCATTTTCT GTTGTGCAGA
22101 TTTATTCAAG AAACCTAATT TTAGGTTGTT GAATAGAAGT TTTGATCAGA
22151 TAAAATTGAA TTAATAAAAA TTTT'TTTTGA GACAGGGTCT TGCTGTTATC
22201 CAGGCTGGTG TGTAAGTGGT TGATCACGGC TCCCCGAGC CTCAACCTCC
22251 TGGGCTCAGG TGATCCTCCC ACCTCAGCCT ACCGAGTAGC TGTAACCTACA
22301 GTGCATGACA CCATACCAGG CTCATTTTGT TACATTTTTT GTAGAGAGAG
22351 GGTTTTGCCA TGTTGCCCAG GCTAGTCTCA AACTCCTGGC ATCAAACAGT
22401 CCTCCCACTC TGGCCTCTCA AATGTTGGGA TTACAGGCAT GACCAGCCAA
22451 TTATTTCAAG GAGTTATTTT TTTTCTCTA CTTTGGGGGA AGATGAATTA
22501 TATAAGTCTC CATT'TTAGGA GTATTTCTAC CAAAAGAACT ATTATCTTCA
22551 AATATATTTT TGGATAGTAC TATAGATATA CTAATTTTTT TTTAAATTTT
22601 TAGTAATTTT TTTGAAGATT TTGTATAGCT GTCCAAAGCC AATTTCTGTC
22651 TACCTAATTT CAGCAAGATT TCACTCTTTT CATGTTACTT TTGTCCAGA
22701 ACAAATTTCA AGTGCTTTCT CTTACCTGT GCATTCTTCC CCCTGATTAG
22751 TCTCTGGCTT TGTATTACTT TCAGTCAGAG ACGACTTTTT TTTT'TTGAGA
22801 CAGGGTCTCA CTCTGTCACC CAGACTGGAA TGCAGTGGCA CAGACAAGGC
22851 AGCCTTGACC TTCTGGGCTC AAGCAATCTT CTTTGCCCTC AGCCTCCTGA
22901 GTAAC'TGGGA CCACAGGCAC GTTGCCACCA TGCC'TGGCTA ATTTATTTTA
22951 ATTTTATTTA TTTT'TGAGAC AGGGTAT'TGC TCTGTCACCC AGGCTGGAGT
23001 GTAGTGGCAT GATCAAGGCT CACTGCAGCC TTCACCTCCT GTGCTCAAGC
23051 AGTCCTCTCA CCTCAGCCTC CCCATTAGCT GGGACTATAG GTCCACACCA
23101 CTACACCAGG CTAATTTT'TG TAATTTT'TTG GTAGAGACAG GGT'TTCATCG
23151 TGTTGCCTAG GCTGGTCTTG AGCTCCTGGG CTCAGCGGAT TCACCTGCCT
23201 TAGCCTCCCA GGTGTGAGCC ACTACACTCA GCCTTTTAAA ATTTT'TTACA
23251 GAGATGAGT CTTGCTTTGT TGGCCAGGCT GGTCTAAAA TCTTGGGCTC
23301 AAGCAGTCCC CTCTCCACAG CCTCCCAAAA TTCCGGGATT ACAGGCGTGA
23351 ACTTCGGTCA TTTCTTA'ACT TTTACCCCTC CTAATGACAC TCCAGAGCTT
23401 ACCTTCTTTA CTTT'TGCTTC TTAAGTTAAC TAATAGACAA TTATTGTATG
23451 TGGATATTGC ATTAAGTTGT CTTAGGATAC CCTTTTCAGA GGAGGACAGC
23501 TTTTGACAAA TTGCTGTGCG GGA'AAAAAAA AGTATTTGGC AATTAAGAGT
23551 TGCATTTACT GAAATCTCTG TTGAGAGAGG GGAAGTTACG TTGTCTCTAA
23601 AAGAAAAACT AAAAAGAAAT GGGGAAGTTT TAGCAAAGTT GTTAAAGCCT
23651 GACACTTAAG TCATACTACC TAGTTT'TGAA CTCTTAGCCC CTGCCACAGA
23701 CACGGCAGCC CCTTGAACCT TCCTGGGTTT AAGCGAGCCT CCTACTTCAG
23751 CCCCCTGAGT AACTGGGACC ACTGGCCTGT GTC'ACTGTGC CTGGCTAATT
23801 TTTTTTTTTT CCTCACATGG GCAATGTTGG GCAAGTTAAA TCGACTTCTT
23851 TGTGCCTCAG TTTCCTCATC TGAAATGGAG ATCATACTGC TATGTACCTG
23901 ATACAATGTT TGTGAGGATT GAATGTGCAG AGTTCTTTT TTCTGTTGTT
23951 GTTGT'TTTGA GACGGAGTCT CACTCTGNNN NNNNNNNNNN NNNNNNNNNN
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TCTCGTGATC
24101 CGCCCGTCTC AGCTTCCCAA AGTGCTGGGA TTACAGGCAT GAGCCATCGT
24151 GCCCGGCTGA ATGTGCAGAG TTCTTAA'AAAC CGTGTC'AGA ACATAAAATA
24201 GTTATTTGTT CTTT'CATATA ATGATGATTT TGAGGGCCTG CGGATCTTGA
24251 CATGTTATCA GATTGGTCAA AAAAAGATTA AACCATAGTT GGTATTGTCC
24301 TAGTTCCTGT TACCAGAATA TTCCATCTTT CATCGTTGCC TTCTCTCATA
24351 GTTTTATGTA TCAAAAAGTT TATTGTAAAG CTAGGCCGGG CACGGTGTCT
24401 TGGGCTGGTA ATCCCAGCAC TTTGGGAGGC CAAGGCTGGC AGATCAGTTG
24451 AGGT'CAGGAG TTCGAGACCA GCGTGGCCAA CATGGTGAAA CCCCCTCTCT
24501 ACTAAAAATA AAAAATTAGC TGGATGTGGT GGTGGGTGCT TTAATTCAG
24551 CTACTCAGGA AGCTGAGGCA GGAGAATCAC TTGAACCCAA GAGGCAGAGG
24601 TTGCAGTGAG TTGAGATTGT GCCACTGCAC TCCAGCCGAG GGGACAAAGT
24651 GAGACTTGAT CTCAAAAAAA AAAAA'AAAAA AAAGTTATTG TAAAGCTAGA
24701 CACGGTGGTA TTTGCCTACA ATCCCAGCTG TTCGGGAAGC TGAGGCAGAA
24751 AGATTGCTTG GGTCCAGTAG TTTGAGTCTA ACGTGGGCAA ATATATGAGA

FIGURE 2H


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24801 CTCCATCTCA AAAAAAAAAA TAAAAAATAA AAATAAAAAA ATGTTTACTA
24851 GTTTTTTTTCA GTAGCCTTTT ATTATAGTAG CAGTACATGT GTATTGTAGA
24901 AATTTGGAAA ATACAAGTGA AAAATAAAAA CATCAAATTC CCGTCAGCCA
24951 GAGACTGCTG TGAAATGTTT TGAGCACATC CTTCTTGAAT GTTTTTTAAA
25001 TCCTGGTATG TATATTTGTA TTTTAAAATC AAAATGCATT CTTACCCATT
25051 CTCTTTTGAA CCTGCTTTT TGTAGCTAAT GATCTCTAGT GTGTCCATTT
25101 CAGTAAAAAT TCCATTATTA AAGTGCTTTA AAAATCGTCT CTTACAGTAC
25151 TGCCACTATG TTGCTGGGCT GGTGGAATT GGCCTTTCCT GTCTTTTCTC
25201 AGCCTCAGAG TTTGAAGACC CCTTAGTTGG TGAAGATACA GAACGTGCCA
25251 ACTCTATGGG CCTGTTTCTG CAGAAAACAA ACATCATCCG TGACTATCTG
25301 GAAGACCAGC AAGGAGGAAG AGAGTTCTGG CCTCAAGAGG TAACAGATTC
25351 AGGGTATTTT GGGGAAAAAT AACTTTAGAC ATTCTCTGAA AAATCCTTTA
25401 ACTCTTGTGG TTGCGGTGGA TGGCGGTGA CAGAAAAACA AGCCAGGCCT CCCCCAGGCA
25451 GCATAAGGGG ATGTGGAAAA TAGGATAGAT TGACATGAGT TTGCTTCAGG
25501 TAGACTGGCT GACTCCCAGG ATTCACACCA CGTAATCAGT ATATTCAAGC
25551 CTTGCTGTCC TTGATTTCTT TCAGACGGTC TTTCTCCAAG TGGTGGATAT
25601 GGTAAACAACC CACGTGCACT AGCTTAACAA AAAGTTCTTA GGAATGGCTT
25651 TGTTGCGCCT GGCGCAGTGG CTCATGCCTG TAATCCCAAC AGTTTGAGAG
25701 GCCAAGGTGG GCGGATCACC TGAGGCCAGG AGTTCGAGAC CAGCCTGGCC
25751 AACATAGTGA AACCCGTGT TACTAAAAA ATACAAAAAT TAGCCGGGCG
25801 TGGTGGCAAG GGCTTGTAAT CCCAGCTACC TGGGAGGCTG AGGCAGGAGA
25851 ATCGCTTGAA CCCAGGAAGC AGAGATTGCG GTGAGCTCAG ATTGTGCCAC
25901 TGCACTCCAG CCTGGGCGAC AGAGTGAGAC TCCCTCTCAA AAGAAGAGGA
25951 AGGGCTTGGT TCTTCTGCTC AGCCCTGAAT CAGTTACTGT TGCTACACAG
26001 CTGAGTTCTC TGGCCTCACC TGGATTACGT CTACACAGTA CACACAGAAT
26051 GGATTTCCCC CAAAGAAAGA ATTCTGCGGC AGGAAGGGGA AAGGGATGGC
26101 AGGTAGACAA AAACTCCAGG TGTCTGTAAT AAGGGACAGG GTCGATCTTT
26151 AATTAAAACA TGGACAGGGA ACAGAAAGCT TTTGATACTG ATTTTGTTCa
26201 GAAGGAAAGT AGAAAATTTT ATGACTGTTC CCTGAATTTA TTCCAGCATT
26251 TACCTTTTGC TTTCATAAAA AGTGTTTCCT GCAGCCAAGT ACTTTAAAGT
26301 TTTAAAAAGA CGGGTGAGGC TAAGTGTGGT GTCTCATACT TATAATCCCA
26351 GTGCTGAGGC CAGGAGTTCA AGACCAGCCT GAGCAACACA GCAAGATACC
26401 ATCTCTATAA AAAATTGTTA GAAAATGATT CTGCTGAAAG AGCAAAAAATA
26451 AAAATTAAAG AAAGTAGAAA AAATAAAACT AAATTTAAAA GATTAAGTGG
26501 GCATGTTGGC ATGCACCTGT ATTCTAGGT ATTGCGGAGG CTAAGGCACA
26551 AGGATCCCTT GAGCGCAGGA GCTCAAGGTT GGATTGAGTT GTAATCACAC
26601 CACTGCACTC CAGCCTCGGT GGCACAATGA AACTGTCTCA AGAAAAAATA
26651 AAAGTGACAG AGGGAAACAA TATTTGCAAT TCATAGAGCA GATACAGGGT
26701 TCATATCTCT AATATTAATA AAAACTTCTA AAAGTTAAGA AAAAGGCCAA
26751 CTGCCCCACA GAAAAATGGG CAAGGAGATA AGAACAAAGT TGTTTCACAGG
26801 AAGAGACACA CAGATGATTA TTAATAATCT GAAAAGATGC TGAGTCTTAC
26851 TCCTAAGAAA AATTCACATT TAAACTACTC TGGGGGCTGG GCAAGGTGGC
26901 TCACGCCTGT AATCTCAACA CTGGGAGACC AAGGCAGGAA GATCACTGAA
26951 GCCAGGGTAT CGAGACCAGC CTGGACAACG TAGTGAGACC TTATCTCTTA
27001 AAACAAAACA AAACAAAACA AAACAAAAAA AACAGTAAAA ATTGGCCGGG
27051 CACAGTGACT CTGCCTATA ATCCAGCAC TTTGGGAAGC CCAGGTGAGT
27101 GGATCACTTG AGGTCAGGTG TTTGAGAACA GCCTGGCCAA CATGGCAAAA
27151 TTCCGTCTCT ACTAAAATTA CAAAAATTAG CCAAGTGTGG TGGCATACGC
27201 TGGTAGGGCC AGCTACTTGG GAGGCTGATG TGAGACTCCA TTTAAAAAAA
27251 AAAAAATCAA AATTAGCTGG GTATAGTGGC ACACCCCTAT AGTTCTCGCT
27301 CCTTGGGAGG TTGAGGCAGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT
27351 GCAGTGAACC ATGATCACAC CACTGCATTC TAGCAGCCTG GGAGACAGAG
27401 CAAAACCCTT GTCTCAAAAC AAACAAACAA CAACAAAAAC AAAAAACACT
27451 TCCCTCAGCT CAGACATGGC CTTTTAAGTT TCCTAGGTGA CTCGTGTGCA
27501 GCCAGGGTTG AGAAACCACT CTTGTCTTAC CCCTCTTTTG CAGACACAGG
27551 GCTCAGAGAA GGAAGGGGGA TTGTCTGGGG ATGTATAGTG AGGCAGTGGC
27601 TGCCCTGGAA GTGGAGTCTC AGTCTCCCGG CTCCTAGGCC AGCCCTGAC
27651 CACTGTTCCA TTGTCTCCCA GACAGAACAT CAGCCACGGG CATGTGATGC
27701 ATGAGCGTGA GGCACACCAT CTTGCACACA CAGGAGCAGA GCCCTGCTCT
27751 TCTCATTAC TTACTTTATC TGTAATAATG CATCATTTCT ACCACACGGT
27801 GGTGGTGTGA ATAAAATGAG ATGAACTTCT AGCATAGAGT GCTTAGTAAA
27851 GGTCTGAGAC ATTTCTGATG AGTTGAATCA TGCCAAATGT GGTCTTAGGT

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FIGURE 21

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

27901 GATTGGCTTC TTTTGCTAGC ATGTTTTTCAG GGCTCCTCCA TGCTGGGGCA
27951 TTGCATCACT GCTTTATTCC TTTTATATCGC CTAGTATTAT TCCACTGTGT
28001 GGATAGACCA CATTTATCCA TTCATCAGTT GGAGGATATT TGGGTCTCTC
28051 CCATTTTTTTT TGCTATGGT GAATAGTACT GTGTACATTT GCATATAAGG
28101 TTTTGTGTAG ATGTGTGTTT TCCTTTTTCTT TGGGTCTATG CTGAGAAGTG
28151 GAATTGCTGG TTCATACAGC AGCTCGAACC TTGTGAGGAG CTGCCAGACG
28201 CTTTTCCAAG GTCGCTCCAC CATTTTACAT TCCCGTCAGC AGTGTGAGAG
28251 TCCCAGTTTC ACCAGCACTT GTTGTTATCT CTTTTTAACT GTATGTATAT
28301 ATACTTAACA TTTTATTTAT AATAAATGTA CATAATAGAG AATTTGCCAT
28351 TTTAACTATT TTTAAGTCTA TTATTCAGTG GCATTAAGTA CATTAAATGAT
28401 GTTATATAAC CATCAACACT ATGTTTCCAG AACTTTTCGCT AGCTTCAGAG
28451 AATCCTCTAA ATAATATCAT TAAAAATCAT CAAGCCGAAT CCCACTGTTA
28501 GAATTAAAGG TTTTATTCCA CTTTCAAGTT ATCAGGATCC AGGGAGGTGT
28551 AATACACCTTA GAGGATAGAC TCAGCTCATT TCCCAGCTAT GCCTTTCAGC
28601 AGCATTCTTA CCAGAGTAGG AATATAATGT TAGTCATTAT TTAGAGGCCT
28651 GGCCATCTTG AGAAGGTTTA CTGTTTAGTC TGCAGTACAA TTATAACTGT
28701 TTTTGATATAT TGGGTTATTT TTTTCAGAAG TAGGCCAGTA GCTCTAACAG
28751 GAGCCTCTTT AGCCTGAATT CGTCCAAGTA GTGCAGTGTT GCACTAGTTG
28801 TCCCTCGGGA CATGCTCCCC AATACGTAAC TCACTTCCAG GTTGCAACTG
28851 GACACTTACT GGTAGTCAGA AATAGCTATT GCATGGAGCT TAAAAAGAAC
28901 TTGATCTTCG TGAAGAGTGA GTCTGCAGCT AAGAGACTTT ACTGTATATC
28951 ATAGTGTTTT TTTTGTTTTT GTTTTGTTTT TGTTTTTGTG ACGGAGTCTC
29001 ACTCTTTCAC CCAGGCTGGA GTGCAATGGC GAGATCTTGA CTCCTGCAA
29051 CCTCCGCCCC CTAGGTTCAA GCAATTCTTC TGTCTCACCC TCCTGAGTAG
29101 CTGGGATTAC AGGCGCCTGC CACCGTACCC GGCTAGTTTT TGTATTTTTA
29151 GTAGACACAG GGTTTACCA CTTTGGCCAG GCTGGTCTTG AACTCCTGAC
29201 CTCGTGATCC ACCCTCCTCG GCCTCCCAA GTGCTGGGAT TACAGGCGTG
29251 AGCCACGGCG CCCAGCCTGT ATCATAGTTC TTATGCACAA AGACCCTTTA
29301 ATATTGTTTG TAAATTCTCC CCTATGCACA CGCTGACCTG TTCCTTAATC
29351 TTCTTATCTG TCTAGGTTTG GAGCAGGTAT GTTAAGAAAGT TAGGGGATTT
29401 TGCTAAGCCG GAGAATATTG ACTTGCCGT GCAGTGCCTG AATGAACCTA
29451 TAACCAATGC ACTGCACCAC ATCCCAGATG TCATCACCTA CCTTTCGAGA
29501 CTCAGAAACC AGAGTGTTGT TAACCTCTGT GCTATTCCAC AGGTAGGGAA
29551 CGGGGCTCCT CTGGGTGGAT ACGGGGCTAA AGGGAGTGGG GTAGGAGTAA
29601 GGGTGGATTT TGCTGTGCTA TATTCAAGGA TATGATTCCT TAAAAAGACG
29651 ATGACTCCAG TTTATTACGC TGGGAGTTTC ATAGCACCCG CCTTTGCTTC
29701 CAGCCACCAA ACTCAGCTCA GCCTTGAGGT TAAGCCTGCT CCTTTTCAGA
29751 ACCTTCTTTC CGGATTTACT ATTTTCTACA GCTATCCTAA ACTAGTTAGG
29801 TTCTTTCTCT CACAGTTAAG TCAAGGTCTT TGGCTTAGAT TTATGGGGAG
29851 TGCTGGGTAA AACCTGGGTG AAGCTGTTAT CATTAAAAAG TCTTCATTAA
29901 GCACCTAATT ACTGCTGTCC TTTTCCTAGA CCCGGCATAA AAAGAACCCTG
29951 GTCCGGTAGA CCTAGCCTCT CAGTATGCTA GGAACCTACA CTTTTTAGTT
30001 GCCTTTACCA AGTATTGCAG ATACTACTGC AAATAAGTGA AGAAAGTAAC
30051 AGCATTAAAC TGATTTGGGA ACTTGGTTTG ATCTTGTTCT AATGACCCAC
30101 TTCGAATGGT GGTGAAAGT AAAATCTGTA TCGCCGTCTT ATGTTTCCAT
30151 TTACCTAGAA ATACTTTACC TTTGAGCACA GGAAATTAAT CCCCTTCTGG
30201 TTGTTCTCCC CTGGCATTG GTTTTAAATA TATAATGATT ATGTTTGTG
30251 TAGGAAAAAT AGAAAAACAA CTACAATAGA AAATCTTCC CATATATTAT
30301 TTTGAAATAC ATATTCCGA TCCGATAATC CATTGCTCTA GCATGGAAAA
30351 TGTTGGATTT ACTTGTGTTT GCTTTTTCCA AATAAAATGG AACTTTTGTG
30401 GCTACATTAT AGAATTGTTT TAGACTGCTT AATTCTGTGT GTTGTGAGA
30451 AAGGGAGGAG TGGGAAGGT AAAAATCTTG ACATACTTTC TTCGTGGGTA
30501 TTTTTTCTTG AGCGATTCCA TCTTAGTTGA TTAGCAGTTA GCAATTGCC
30551 ATTCAACAGA AGGTTTTCTT ACCTTTTTGT GATAATGATA GCTAACGACA
30601 TCATTTCTTC TTTTTTCCCT CTCTTCTTGT TGTCTCTAGG TGATGGCCAT
30651 TGCCACTTTG GCTGCCTGTT ATAATAACCA GCAGGTGTTC AAAGGGGAG
30701 TGAAGATTCG GAAAGGGCAA GCAGTGACCC TGATGATGGA TGCCACCAAT
30751 ATGCCAGCTG TCAAAGCCAT CATATATCAG TATATGGAAG AGGTGGGTTT
30801 TTATTTAATC ACTTGGATAA TTTGTAGCTA CTTTTATGAT TTAGTAATGT
30851 CACTGTTTAA CCAGGTTTGG ATATTAGATG ATCCTAACAA TTCCTATCC
30901 TGTGGCCTAA AGAGACAGGA ATTGATATCC TTTATAAGGA AAAAAGTCTA
30951 TTCACAGGAG CCGAGCAGAT TGCTCACTGC TGTGTAGTAC CCTGGTGAGA

FIGURE 2J

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

31001 GGAGATAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCTCAG TAGAATCATA
31051 GATTTTGAGC TGCAAGATGA TGCAGGAGGC CAACCAAGCT TCTTGTGCT
31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT
31151 GAGTGGATCT CTGGCTCCCC TCCATGTGTC CTGACACCCA GTCTGGTACT
31201 TTCATTATGC CACAGGCCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC
31251 CAAGGAAAGC CATCAAGTTG CAATTATTTT CTAAATTTTC TTTGGAAAAT
31301 TTCATTTCAA ATACCAAAAC CATCCTATAA AAAGAAAAC TACCTTCTTA
31351 GGTCAAATCT CTAATATTTG ACTAGGTTCA AAAAGTTTAT TTCTGGCCAG
31401 GCACAGTAGC TTAATCCTGA AATCCCAGCA CTTTGGGAGA CCAAGGTGGG
31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG
31501 ACCCCATTTT TACAAAAAAT TTAATAATTTG TCATGGTGGT GCACGCCTGT
31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGGATCACAT GAGCCTGAGA
31601 GGTGAGCATT ACAGTAAGCT GTGTGATTTT ATCATTTGCAC TCTAGCCTGG
31651 GTGATAGAGT GAGACTTTGT CTCAAAAAAA AAAAAAATAA AAAAAAGTCTT
31701 AGAGACCAGA AGTCTCTGTA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG
31751 TGGTTTGTA ATGGAGGTGA TTTGCTCCCC TCCCCCAGA GGACATTGGA
31801 CAATGTCTGG AGACATTTTT GATTGTCCTA ACCGGCAGGA ATCGGGTGCT
31851 ACTGGCATCT GGTGAGTAGA GGCCCAGGAT GATGCTGTGA TCCTCAGGTG
31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAA CATAACAAGC
31951 CCTCATCATT TTTCTTTTGC CTGAGCTCCC TCCCCAGAGG TTACCTCTGT
32001 TCATGGTTTT GTGCATCCGT CTAGTCCCCC TGTTACGCGT TTACAGGAAT
32051 ATGGTTTGCA ACAGTGTTTT CATCTAAATA GAATTATACA AAATAGCGAT
32101 TTCTGATTTT TCTTGCATAT TGCACATTCT TCTTATACTT CCTCCCTACC
32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAACCTCTAT CAGAGGCACC
32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAAACC CTAAATTTT
32251 GTAGTCACTA GATGAAAATA TTCAGCCAGT GACCCAAAAA ATTGCTACCA
32301 ATGAGACTCT CCATTTTGCC ATGTAGCCAG AACTTACTTT GATCTATGTG
32351 CCTGGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG
32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA
32451 CATCAGAATC CATGATGTTA ACCCCAATTC TAAGGGGTTC AACTACCCCT
32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCAT TTTATATAAA
32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTTTTG GTTTTGCACT
32601 TTGATCACTA GTTTTAGAAA CCAGTTTTTA AACACTTTGT GGCCAATTCC
32651 ATTACTATAT TAAATTCAG ATTTATTTGG TTTTTCCTTA ACTATTGGGA
32701 TTAATCCTG GTTGTAATTC ATAGTTTGAG GCGAGGGTG GGCAGTCTAC
32751 ATTTGGCTGA GCCCTGTTTT TGTGAATAAA TGTTATCAGA ACACAGCCAC
32801 ACCCATTTGC TTCTATGTCT TCTGTGGCTG CTTTTGCAAT GTGACGGCCG
32851 AGTTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTTT
32901 GGCCCTTGAA TAAGAGGTTG GCTGACTTCT GACTTAGGGC ATCAGTTGTT
32951 CTGTTATCCC AGTAAAACTC AAGGCATTAG GGGAGAAATG TTAATATTAA
33001 TACTTAAGTT GATTTGATTT AGGGAAATCT TTGAAGATTT CTAAGTCTTA
33051 AGCAGTAGAA CCTGTTAATG GTTTTAGTTT CAGCAGTAAG GACATTTTAC
33101 AAGTAAAGTT TTAATGAAA ACATTTTGTA TGAAGCCACA AGTCGTCTGG
33151 CCTCTTGCTG GTGTCCAGAT ATTAACACTG ATCCTATTTT TCCTTGCTGA
33201 CCAAGTCTGT CCTTTGTAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA
33251 TCTCTGGACT TAGTGTTGTA GCGAGCATGC ACCTGGAAGG GACTTGCCAG
33301 AGGACCTCCT CATGCTTCTC CAGTGCTTAG TGGGGGCTTG GAGTGCAGCC
33351 CCAGGTCTTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCACTCT
33401 GGAGCAGCCT CTGCTTCAAA CCAGCCTGGA TGCTTGTCAG CTGGGGAGAA
33451 GATCAACCTG CTATTTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG
33501 AAACCCCAT TCCCCTCTCT GCCAAAGTGA ATTCCTTGGC AGGGAGAAGC
33551 TTGTTCTGTT CTCTGCACAC TTCTGTGCTC CTCCTGTGGT TAAGTCAGAG
33601 AATCATCCGG CTTCTTGAGC CCCAGGTGCC TAGCTGCTCA AGGATGGTCC
33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCATTA GACATCCAGC
33701 CCCCACCCAA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CCAAATGATG
33751 TTTTCTGCTT AATGGAAGTT TAGATGTTCA TAGACAAGAG TTTTAAATGA
33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT
33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT
33901 GCACAAGAGC TTATTTTCAGT CTAGTAAACA TTTATAGGAG CTTGTGTCTAT
33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CCAAACTTT
34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC
34051 TGGCCAATAT GGCAAAACCC TGTCTCTACT AAAAATACAA CATTTAGCCA

FIGURE 2K

34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCCGAG CCTGAGACAT
34151 GAGCATCGCT TGAACCTCGG AGGTGGAGGT TGAGTGAGC TGAGATGGCA
34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTTT CTCAAACCTCC
34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC
34301 TATGACCTGT CCTTGACAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG
34351 GTTTTTAAGA CCTGAATAAT TGAGTTTGCA GAAACCTACT GTGTGCCTTC
34401 AGGTAAATGG AGAGTGGGGT TTGGTCTAGC AACGAAGCAT CTAGAAGGTC
34451 TCTTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCAG
34501 TGACTGCAGC TCTTCCAGTT GTGCTGTCAT GTTTATATGT TAGAAATGAT
34551 CATCAAAGGA CTCAAAGATT TTGCCACTAA TTGTATTACC GGGGACTGTC
34601 ACAACCAAGA TTTCTCTTAA TTTATTCACT TTACTTATCT CCTGGAAGGG
34651 CATATTGAAG TGCTCTTGGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT
34701 ATATTCACCT GGTGGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTTC
34751 CCAAAAGGAT GTAAGATGGC TTATGGTTAT AAGTACAACA GGCTAACAAA
34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAGTCA TAGGAGCCAC
34851 AGAATTAACC CAGGAATGAA TAAGTGTGTA GTTTGGTGCT GATGTTATCA
34901 TCCTTTATTT GTACATTGCT TGTACAGTTG CTCTGAGAAG GTAAGTCTTA
34951 AATTTTCAAA AGTGAAATGT CACCGAGCAT GGTGGCTGAT GCCTCTAATC
35001 TCAGCAGCTTT GGGAGGCTGA GGCAGGCGGA TCACTTGAGG TCAGGAGTTC
35051 GAAACCAAGC TGACTTATGT GATGAAACCC TGTCTCTACT AAAAAAAAAA
35101 AAAAAAAAAA AAAAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG
35151 CAGGTGCCTG TAATCCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA
35201 TGAACCTGGG AAGTGGAGGC TGCAGTGAGC CAAGATTGCA CCACTGCACT
35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAACAAAAA AAAAAAATCT
35301 ACAATATAAC AAAACCATTA CTTACCTGAG AAACATTTCT CAGGGTCATT
35351 GTAGTGAATG CCTATTTTAT GGCTTTTGAT GGCATCAGGG CACTCAGGTC
35401 ATTTACAAGA GTAGTGTGTG AGACCTGTG TGTCACTGCC ACTCATCTTG
35451 GCCTTCGGCC ACTGCTGTAG CAACCAGTTT CCAAGTAGGG CTGGACCTTG
35501 CCTTCTGCTC CAGAGACCTC TCGCTTCCTG CCCTTGGGCT TCTGACGAGC
35551 TGCAAGAACT GCCTGGCAGG TGGGTCCCA CAACCCAGAG GAGGTGAGGG
35601 CCACCTCTCT GCTCCTCAGG GCCACCTTTC ATAAGGCTCC TTGAAGGTCC
35651 CTCAAGATCA AGCCAACCTCA ACACATCCTT GATAGGCCTT CCTGCCTTCT
35701 GTTTCACCTT TCCACTCGTT TCCAAATAAA TGGCTGCATG CAAGCTTTTG
35751 CCTCAGGTTT TCCCTTTTAGG AGGAAGGCTA AGACAAGCAG TAAAGCAACA
35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT
35851 TTTACTTTAT GGATGCTTGT ATTGAAAAGT CTTGGCTGGG TGGAGTGGCT
35901 CACGCCTGTA ATCCCAGCCC TTTGGGAGGC CGAGGTGGGT GGATCACTTG
35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGTCCTC
36001 TATTAAAAAT GCAAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC
36051 ACAGGGCTAG CTGGAGATA AAAAGGTGAG TAAGTAGGTC CGGTGTAGTC
36101 AGGGTGAAAA CTACAGATGG TCCATTTCCA CGTAAGTGGA AAGGTAAAGG
36151 TATGTACAAT AGGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT
36201 TCTAGAAGGC ATAATCCTGA AGTTGAGACT TGGGGGCTTA GGTAGGAGCC
36251 AGTTGAAGGG ACGTGGGAGG CGCATTCCAG AGAGAAGGAG TGGTATGAGA
36301 CTGGAACAGA GGTGTGCAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA
36351 GTTGTCTTTT TGTTTTTGTG TGTTTTTTGA GACAGGTCTT TGTTCTGTCA
36401 TCCAGGCTGG AGTGCACTGG CATGATCTCG GATCACTGCA ACCTCCACCT
36451 CCCAGGCTCA AGTGATCTTC CCACCCAGT CCCCAGTAG CTGGGGGACC
36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTTGTACATT TTGTAGAAAC
36551 AGGGTTTTAC TGTGTTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA
36601 GTCTACATGC CTCAGCCTCC TGAAGTGCTG GGATTCCAAA CATGAGCCAC
36651 TGTGCCTGGC CCGGCAACTG TTAGTAGACT ATAGAGAGGG AGGTGGGCAA
36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT
36751 GCGCTACACA TTACAGAGCT CAGGCTTTTT TTCTCCAGGT GAGAGGGCTG
36801 GTGCCACTGA GGCATCAAGC AGAGGTTTGA GATCTCCTTG GTGACAGTGT
36851 AGAGCAGACA GGTAGATTTG GGAATTTAAG CTTAGACTCA CGTTGGAGAC
36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT
36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTTGT
37001 GGAGGCTGGG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG
37051 CTCCCTGCTT CTGTTCTCTG TCTTCTTGT CAAGCTGTGG TCTGTACTGC
37101 GTGTTCCATC TTGTTTCTAA GCTGCTTTTG CCCAGTCTTT CCAGCATTTT
37151 CCTTCGTCA TGTTAGTCTG TGCTGTCTA CGTGAACAT GGTGACGTTT

FIGURE 2L

```
37201 ATTGGGCCTG GCACTGTGAG GTGCTGGGGA TGTGAAGATC ATTGTGGCTC
37251 AGCCGCTGCT CTCGAGGGCC TCTGGGTGCA GTATGCACAC CTGTGCCTCC
37301 TGTTTGCTCA GGAAGACAGG CTTTGAGATG AGCTGGGGCT GACATCCCCA
37351 CCTTATCATT GGGATGGCTT TGGGTAAGTT ATGTTTCATGT TCTCTGAGCC
37401 TCCCTTTCCT CATTGGTAAA ATGGGTATAA AATACCTGCC AGTGGAGGGT
37451 TGTGTAAAGT AGCCATGGAA AATGTAAAGC ACATAGCACT TACCATTTT
37501 TCCTGTGTCT TTAACAGATT TATCATAGAA TCCCGACTC AGACCATCT
37551 TCTAGCAAAA CAAGGCAGAT CATCTCCACC ATCCGGACGC AGAATCTTCC
37601 CAACTGTCAG CTGATTTCCC GAAGCCACTA CTCCCCATC TACCTGTCGT
37651 TTGTCATGCT TTTGGCTGCC CTGAGCTGGC AGTACCTGAC CACTCTCTCC
37701 CAGGTAACAG AAGACTATGT TCAGACTGGA GAACACTGAT CCCAAATTTG
37751 TCCATAGCTG AAGTCCACCA TAAAGTGGAT TTACTTTTTT TCTTTAAGGA
37801 TGGATTTTGT GTTCTCTTTA TTTTTTTCCT ACTACTTAA TCCCTAAAAG
37851 AACGCTGTGT GCTCGGACC TTTAGGAAAG TGAAATGCAG GTGAGAAGAA
37901 CCTAAACATG AAAGGAAAGG GTGCCTCATC CCAGCAACCT GTCCTTGTGG
37951 GTGATGATCA CTGTGCTGCT TGTGGCTCAT GGCAGAGCAT TCAGTGCCAC
38001 GGTTAGGTG AAGTCGCTGC ATATGTGACT GTCATGAGAT CCTACTTAGT
38051 ATGATCCTGG CTAGAATGAT AATTAAAAGT ATTTAATTG AAGCACCATT
38101 TGAATGTTCC TACTAGTAGA AAATGATGTG AATTTTCTTT CTGTTGCGCT
38151 CCTATTTTTC TCATCATTTT GTTTTCTTTA ATTGGGTGA ATGGAGTAGA
38201 TAGAAATATT TATGGTTTAG GTAACAGTTA GATGTTTCCT AAGAATGCAA
38251 ACTGCCTTTT CCACACAAAG GCTGGGAATA AAATTCTGGG TATTCTCGTA
38301 TTCTCATTTA AAGGAGTTTA GCTTTCAGAG AGAAACAGCA GGATTGCTTT
38351 TGACCTTTTA GAAGATTGGT CTCCAGTAAA GGTGGACATT TTTGAGATTT
38401 TTATAATAAA GAATTTAATT GCTCTGCATT TGTCAAGTAC AGTTCGCTTG
38451 AAAGCCTGCC TGACTGTGGA AAAGATGGAG CTCAAGAATG GAGTTGATGG
38501 CCCAGCGTGG TGGCTCATGC CTGTAATCCC AGCACTTGG GAGGCTGAGG
38551 CGGTCGATC ACGACATTAG GGGATCGAGA CCATCCTGGC TAACACGGTG
38601 AAACCCCGT CTCTACTAAA AAAAAAAAAA ATTAGCCAGG CGTGGTGGCG
38651 GGTGCCTGTA GTTCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCTTA
38701 AACCCGGGAG GCGGAGCTTG CAGTGAGCTC AGATCGCGCC ACTGCACTAC
38751 CAGTCTGGGC AACAGAGCGA GACTCCATCT CAAAAAAGG AAAAAATTGT
38801 AAAAAAAAAA AAAAAAAAAA NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN (SEQ ID NO:3)
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FEATURES:
Start: 2058

FIGURE 2M

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

Exon: 2058-2156
Intron: 2157-7996
Exon: 7997-8094
Intron: 8095-8869
Exon: 8870-9053
Intron: 9054-25147
Exon: 25148-25339
Intron: 25340-29365
Exon: 29366-29542
Intron: 29543-30639
Exon: 30640-30792
Intron: 30793-37517
Exon: 37518-37736
Stop: 37737

CHROMOSOME MAP POSITION:
Chromosome # 8

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
825	G	A	Beyond ORF (5')			
2632	C	T	Intron			
4430	C	T	Intron			
4791	C	T	Intron			
4886	G	C	Intron			
4887	A	T	Intron			
4889	T	A	Intron			
5110	G	T	Intron			
6911	G	A	Intron			
7212	A	G	Intron			
7355	C	T	Intron			
7398	T	C	Intron			
7653	T	C	Intron			
8310	A	G	Intron			
8145	C	T	Intron			
8031	G	A	Exon	45	R	K
8462	G	C	Intron			
8873	C	T	Exon	67	N	N
9190	C	T	Intron			
9311	T	-	Intron			
9847	T	C	Intron			
10460	C	T	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	A	Intron			
21477	G	A	Intron			
22230	C	T	Intron			
22941	A	G	Intron			
23963	C	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	C	G	Intron			
27151	C	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron			
29572	C	T	Intron			
29761	C	T	Intron			
30732	G	C	Exon	281	L	L

FIGURE 2N

30841	G	T	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C	Intron
34532	T	C	Intron
36541	T	C	Intron
36607	A	G	Intron
36681	A	G	Intron
37493	C	T	Intron
37966	C	A	Beyond ORF (3')
37973	T	C	Beyond ORF (3')
38113	C	A	Beyond ORF (3')
38298	G	C	Beyond ORF (3')

Context:

DNA

Position

825	GCAGTGAACGTACCTGACAGGTTTCCTGTTTGTGTTTTGAGATGAAGTCTCGCTCTTGTC CCCAGGCTGGAGTGCAATAGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCTGTGTCA AGCGATTCTCCTGCCTCAGCCTCCCAGGTAGCTGGGATTATAGGCGCTGCCACCATGCC TGGCTAATTTTTGTATTTTAGTAGAGACGCAGTTTCAGCATGTTGGCCAGGCTGGTCTT GAACCTCAGACCTCAGGTGATCCGCCGCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGC [G, A] TGAGCCACCGCTCGGCTAGACCTGACAGGTTTTAAAGGATTACTGGTTGCTGTGTTA AAACAGACTGCAGGATGGCTTAGGTAGCCAGTAGGTTTTTTTTTTTTTGGAGACGTAGT CTTGCTCTGTTGGCCTGGCTGGAGTGCAGCGGTGTCATCTTGGCTCACTGCAAACTCCGC TTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCGGAGTAGTTGGGACTACAGGCCCC CACCACCACACTCGGCTTTTTGTATTTTAGTAGAGACGGGTTTCACCATGTTGGCCAG
2632	GCCGCTCTGGCTGACCTGTCCCTGCCCCGCAAGCCGCCCTGGGCATGAGCGACTTTTGC GTGGTTCCCGGTGGTTGCGCTCCCCGTTTCGTCCCCTCCGTGAGCATCGGCGCTTACCGG TATTTTAAACCGAGGGTTACACATCTGAGGCAATGTGGGTGGGTTACGCGGAGAGGACG AGTGAGTTTTTTGGTAAGCGGAATGAACTATGCAGATAACATCACATGAAGGCCGTTTCT GGAATGAAGTCTGACTCCTCCAGTTTCACCACCTCTTCCGGAGCTCTCCCGCCTTGCTG [C, T] CTTCCATCGCTTCATCCTCGGTGCTTCTGAGTTTTTAAATCGCCTATCTACGCTTCCAA GTTCCAATGAGTTATCTAACGTCTATGGATTAGCTAGGTGGTTGGTGAAGGTCAGAACT TGGTTTTACTTAGATTTTTATCTGCCTCATGCCTGTACTATTTGTTAATGAATGCATAG GAGGTGTTTTTATTCCAACAAGAAAATTATTTCGTACGCGATTATTGAATGAATAGACAAA TTCAGCCAAGTTCTTCTGGTCTGGACCAGCCTGGCTGATTTCTGTAACTTTTTGGGCCA
4430	GGCCTTTTTTTTTTTTTTTTTTGTAGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT GTGGCCTGAACATGACTCACTCCAGTTTGACTTCCTTGGCTGAAGCCATCCTCCACCT CGGCTTCTGATCCCGAGTAGCTGGGACTCCAGGCACGTGTACCAATGCATGGCTAATT TTTAAATTTTTTTGTAGACACAATGTCTCGCTGCATTGCCAGGCTGGTCTTGAATCCT GAGCTCAAGCGATTTTCCACCTCAGCCTTCAAAGTGCTGGGATTACAGGTGTGAGCCAC [C, T] GCACCCAACAGTTTCTCTGCAAACTAGGGAAAAAATTACGCTTAGCAGATATTGAG GGCTGATTATTTCTATCACAGAAGCATTGGCTATAGAATTTAGGGTTTAGTAACTTG ATTTACACTGAATTTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT
4791	GGCTGATTATTTCTATCACAGAAGCATTGGCTATAGAATTTAGGGTTTAGTAACTTG ATTTACACTGAATTTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT AAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAACCTTGGTAACTTAACCTCTGAAC

FIGURE 20

[C, T]
ACAGTTACTTCATCTGTAAAAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAAC
TCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGC
AGCAAAACCTGACTTGAAGTTGAGGCTTCATTATCCCACTTAGTATATTCAAATGTTTT
GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTAT
TGCCATTTTTCTAAACACTAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTT

4886 CTACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA
AGAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTT
AGACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC
AACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAAATAGGGATGTATGT
ATGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTT
[G, C]
AGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCAT
CCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACT
GACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAACACTAAAATGCTAAATTC
TGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT
TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4887 TACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA
GAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTA
GACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA
ACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAAATAGGGATGTATGTA
TGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTG
[A, T]
GTGTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATC
CCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTG
ACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACACTAAAATGCTAAATTC
GCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT
GATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGA

4889 CGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA
GCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGA
CTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAAC
CTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAAATAGGGATGTATGTATG
GTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAG
[T, A]
GTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCC
ACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTGAC
TAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACACTAAAATGCTAAATTCGTC
CCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGTTGA
TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA

5110 AAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGT
CTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAA
GTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATG
AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACA
CTAAAATGCTAAATTCGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCT
[G, T]
TGAGACCTTAAAGGGTTGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA
TGGAGTTAAGTGCTTGATAAATGGTGGTTATCAATCTGATTATGTAAATTTATGTAAATT
CAGTTCTCAAGTTTGTGGTTTTTTCCCTCCTGGAGAAATCTATTCTATTTTAAAGTGA
GGAAGGCTCCGTGGAGGCTGGTAGCTGTAGCTGTTCACTTGTGGAACCTTCAGCCTGA
GGCTGGAGCCCCCTCCTGGGAGTCTGGTCTTGTGCTTCTGACCACCCACACCCCTT

6911 CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCGTGCGCCACTGCACCCGGCCCTGTT
GGATAAATGATTCCAGTCTCTCCAAAAAGAACTGTTGTAAGACTGTGGGGTGAGGGGAG
GGAAGGGACAAATAGGAACCCGCGTATTTTCCACTCCCTGTGGGCCTAAAACCTGCTCTA
AAAAATAGTCATGAAAAAATAACATAGTACAAACAGCAACTCTTCTGATATGCTGTCAT
TAAAAATCAGGCTTTTTCTCCCTTTTGGAAAAACACAGTCCTTGTGCTTTAGGGAAGA
[G, A]
TAAAGGTCAGTGCCTGCATTGCATTAATTTTGAAGGAAAGATGAGAAGACATCTTGAA

FIGURE 2P

AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA
TGGCGGGGAGCCGGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGC

7212 TAAAGGTCAGTGCCTGTCATTGCATTAAATTTCAAGGGAAAGATGAGAAGACATCTTGAA
AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA
TGGCGGGGAGCCGGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGC
[A, G]
TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGG
AACCTAATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAA
TTTAGCAGGATTCTTGGTAAAACCTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTC
CAGGCTTTATTGGGAAGAGGATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACT
CTGTCACTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTCTCTTAGCGGCCAGT

7355 CAAAACAGATTTTATTAGAAAACTACTGCAGTAAGAGGAGAGAGACCTCGGTACAGAA
CTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGGGGAGCCGGATGTCTAGT
GGATGGAATAATTATTACGAGGAAACACAGGGGTGTGCATTCTTGCTGAAGGCAGGCCAGA
GTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCTAATCGGCTGTCTAGGGT
GATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAGCAGGATTCTTGGTAAAA
[C, T]
TGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGGATT
TCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG
CCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAAGGGCAACA
GCGGGAGGAGCGCCGCTGCGGAGCGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGGGGC
GGGCCCGTTGTGGGTGCGCCAGCGCTATTCTAGTAGAGGGCGAGCCCGTCCCGCTCT

7398 GAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGG
GGGAGCCCGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGCATTCTT
GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCT
AATCGGCTGTCTAGGGTATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAG
CAGGATTCTTGGTAAAACCTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGC
[T, C]
TTATTGGGAAGAGGATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCA
CTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTC
TGGTGAGAAGGGCAACAGCGGGAGGAGCGCCGCTGCGGAGCGGGAGGCGGGGGCGGGG
CTGCGGGGCTGCGGGGCGGGCCGTTGTGGGTGCGCCAGCGCTATTCTAGTAGAGGGC
GAGCCCGTCCCGCTCTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAA

7653 AACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGG
ATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC
GAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCCTGGTGAGAAGGGCA
ACAGCGGGAGGAGGCGCCGCTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGG
GGCGGGCCGTTGTGGGTGCGCCAGCGCTATTCTAGTAGAGGGCGAGCCCGTCCCGCC
[T, C]
CTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAACTCCGCGGGGTCCGC
GATTCCCATGGCCGAGCCGCTGCGGCACCAAGGCCATGGCCCTCTTCAAGCGCACCTT
GGTGTGAGTCCCGCCGCGCGCCAGGGGCCCGGGCGCAGGCACCGCCCGCGGGGCTG
CTGCTTGCTCTGCGGCTGGCCCTGCAAGGACTGGCTCGGGGAGAGGGCGGCAGGCT
GTGGAGCCGCTGCCCCAGTCCAGTCCCACTCCCACTCCCACTCCCACTCCCACTCCCTG

8310 CAGCCTGAAAACCTTGCTACAAAGTATCTCAATCAGACCAGTCGAGTTTCGAGCTGTTAT
CCAGGCGCTGGATGGGGAAATGCGGTGAGTGATGGAGGCAGCGCTCTGGCTTGGAGGAA
AGCTTGTCCGGGACTTTTGTAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTG
CAGCCTCGTTGCTGTGGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAA
GCCCTTCCAGGCTCTTTGCCATCTAGTAGAGTCCCTGCGGGCCAGCCTTTCAGAGAAG
[A, G]
GGGGGAGGGGGTGATGTTTATTAACCTTTTGTAGTCTTGGCAGCTGAACCTGCCTGTGA
GCAGGTGCTGATTTCTCGGCTTCCCTTATCCAACCTTGCATTTCTATTTCTAGCATATT
GGGTGATTCTTTTGAAGTGCCTCTGTGCACATTACACCCATGAACCTAGACCAGTTGC

FIGURE 2Q

CTTTATGTATGATCGTATTTATACTGAGAAAGTTACTGTGTTTTTTGACTTTCTTTTCTAT
TTGCTACATATTAGTTCGGTCTAAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTG

8145 CAGCCTGAAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT
CCAGGCGCTGGATGGGAAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGAGAGAA
AGCTTGTCCGGGAC
[C, T]
TTTGAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGT
GGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCAGGCTCT
TTGCCATCTAGTAG

8031 CAGCCTGAAAACTTGCTACA
[G, A]
GTATCTCAATCAGACCAGTC

8462 GCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGTGGCTTATCCAGAACAT
AGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCAGGCTCTTTGCCATCTAGTAGAG
TCCCTGCGGGCCAGCCTTTCAGAGAAGGGGGGAGGGGGTGATGTTTATTAACTTT
TTAGTCTTGGCAGCTGAACCTGCCGTGTGAGCAGGTCGTGATTTCTCGGCTTCCCTTATC
CAACTTTGCATTTCTATTTCTAGCATATTGGGTTGATTCTTTTGAAGCTGCCTCTGTGCA
[G, C]
ATTACACCCATGAACTTAGACCAGTTGCCTTTATGTATGATCGTATTTATACTGAGAAGT
TACTGTGTTTTTTGACTTTCTTTTCTATTTGCTACATATTAGTTCGGTCTAAACGTTTGG
TCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGGAGTAGTGGTG
ACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCATGTAAGGAAG
GAAACTAATGTAACCTTCGTTAAGTATGAAAAGCGTTGGATATCCTTATAGTTCTTTAG

8873 AAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGG
AGTAGTGGTGACATTCACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCA
TGTAAGGAAGGAAAACATAATGTAACCTTCGTTAAGTATGAAAAGCGTTGGATATCCTTAT
AGTTCTTTAGAGTTAAGGGTGAGATGGGTTTAGAAAGTGGCCAGGCACAAGTTATTTTAA
AATAAAAAATCTTTGGCTGTTTGTTCGAATATATTAATAGTTTTCCCTTTTTTACAGCAA
[C, T]
GCAGTGTGCATATTTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACC
ATCAGTGTGGAAGAAGGTCCCGCTGTACACAACCTTCACTCTTTCCTTTACCAACCA
GACTGGCGGTTTCATGGAGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACG
GTGAGTGGGGTTACGCATCTTGTCTACGACTGTTGTGTTTCATAATTGCTAACGTGGTTG
TCCGGTAGCCTCCATACATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTC

9190 ATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACCATCAGTGTGGAAGA
AGGTCCCGCTGTTACACAACCTTCACTCTTTCCTTTACCAACCAGACTGGCGGTTTCATGG
AGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGC
ATCTTGTCTACGACTGTTGTGTTTCATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATA
CATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTC
[C, T]
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG
TAATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCT
CTTAGAATGTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTCCTGTG
GGAAGACGCAGTCAAATTTTAGTGTTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTG

9311 GAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA
TCTTGTCTACGACTGTTGTGTTTCATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATAC
ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTCC
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG
[T, -]
AATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCTC
TTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTCCTGTG
GAAGACGCAGTCAAATTTTAGTGTTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTGC
CGACTGTATGATGCAGCCTACCTGTAACACTGCTGGCCTCTTGACTACCCGGAGCCTGGT
AGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGCGGTGTCTGTTGGCA

FIGURE 2R

9847 CTGGTAGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGGCGGTGTCTGT
TGGCAGCTAGGGCGAGCCTCTGCCACTTCACCTGTGATCCTGGGCAAGTTCCTTATCTGC
TTTGTGTCTCCGTCTCCTCGTTTGTAAAGTTAGAGCTGAGAGGATTAATTTTCGCACATAT
AAAGTAATCTAGTGCCTGGTACAGGGTAAGTATTCTGTAAGTATTAGCTATTTGGTCTATT
TTGTTGGAGTAAAGTGGGTATAGTTAAATCCTAAGATTTTTAAAGTCCCTCAAGTTCA
[T, C]
GTGGACATCTGCCTAGGTCCTACTATCCTAGAATTCGCATGTCTTATCACACAAATAACT
GATTCTTCCATATCTTATAAATAAAGGTTTGATTAGCAAAGTCACATGTTGTGTAATAG
CTCGAAGAGCCCTTTTGTCCACAGTTGCCAGAGCTTTTGGAGAACAGTCCTTATGTTA
TTGAAACAAACCTAATCTGTAGCTGAGTTGGGAGGGAGCTAAGTGGACAGAGAGTCCTCC
ACCCAAACAAAAGAATCTTTGATTCTTGGGCATAATGGGAGCAATATTTAAAAA

10460 AGGAATGTTTGGGGAAGACTCTTGCGGTGCAAAGGCTGTTTCAGATTGCTGAGATCAGAC
CTTAAGTACCAAAGCCCAAATATAGTACAACATAATACAAATGAGAAGAAAATAGCTGAA
GAATAATTCGAGTTTATACAGTACAATTCAAGAGAAGAAAGAAAATTTATGACGACTAGC
TGGGTGAGAATTAGAACTGTAACCTGGGAAGGTCCTGGTGATTGACTCTCACAGGACA
CCTGATGACCAGAGGATGGGTTTCTTTGATGGGAAATCTGTGGCGATTTCATTGATGGGC
[C, T]
TCTGAATCTGCTGAAGCAGAGGAAGTAGTAATACCCATTTATAATGGAAGTGCATTCT
CACTTAAAAACAATAATATTATTCTAGCTGGACCTAGCCTCTAGAAAACAGCCAAATTAC
ATTTGACTTGAGTGGATTCAATAAATAAAAAATTTCTGGGCGATGGGATAAATGTGTT
AGGTATTGCTAAGTCAAGGCAGCCCTATCCCCTCAGCAGAAGTGAGGGAATATGAAAGTG
TGTGAATGCTAACATAAATTTGGGGAATATCGCCGTCAGATTTCCAGATGATATCCAAC

20204 TCTGCCAGTTGCGAAGACTGGGAAAAGCACAGTATTTGGGCAGAGTATACTGTTCTCCA
GGTACAGTCACTCACGCCCTTCTCTGGCTAGGAAAGGGAATCCCCTGACCCCTTGCACT
TCCTGGATGAGGTGACGTCCTGCCCTGCTTTGGCTCACCCCTCCATGGGCTGCACCCACTG
TCCAACCACTGCCAATGAGATGAACCAGGTACCTCAGTTGGAATGCAGAAATCACCCAT
CTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGCTGTTCCCTACTGGGGCATCTTG
[G, A]
AGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGATGTATATCCCCAGTGCCTAGAAT
GATACTTGTATACATAGGAAGTGCTTGATCCATGTTTGCACAAATGAATCTTTCTCATAAT
GAGGTTTCTTAAACAAGCTGTTCTCCCAAAACTTACACCCAGCTTTATGTTGAAGCAT
CTCATTATACATTGGAAGATGAAATGTGTAGTGAGACTTTGAATCTTCTTTTGAATCTA
GAAACATTAGCATTTTGTAGACCATTCTATTTTAATATTTATGAAATTTATGAAATAATAA

20362 CCTCCATGGGCTGCACCCACTGTCCAACCACTGCCAATGAGATGAACCAGGTACCTCAGT
TGGAAATGCAGAAATCACCCATCTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGC
TGTTCTCTACTGGGGCATCTTGAAGCAACTCTGGGTCTGAGTTTCTGTTTGTGCTGCTGA
TGTATATCCCCAGTGCCTAGAATGATACTTGTTACATAGGAAGTGCTTGATCCATGTTTG
CACAAATGAATCTTCTCATAATGAGGTTTCTCTAAACAAGCTGTTCTCCCAAAACTTA
[C, A]
ACCCAGCTTTATGTTGAAGCATCTCATTATACATTGGAAGATGAAATGTGTAGTGAGAC
TTTGAATCTTCTTTGAATCTAGAAACATTAGCATTTTGTAGACCATTCTATTTTAATATT
TATGAAATTTATGAAATAATAAGAAACATGAGGCCGGGCTCAGTGGCTTATGCCTGTAAT
CCCAGCAGTTTGGGAGGCCAGGGCTAGTGGATCATGAGGTCAGGAATTTGAGACCAGCTT
GGCCAACATGGTGAAACCCCACTTCTACTAAAAATATAAAAAATTAGCTGGGCGTGGTGGT

21166 TAATTCGCCCATGTTTGCCTTGTGATCTTTGGTGCCATGTCTGTACATATTTTCATGATT
TCTGTGTTTTTACGGTTTCCATTTAGATCTCCCTTGTGTTTAGAAATCTGGCTGAGAAA
TACCAAACAGTGATTGCCGACATTTGCCGAGAAATGGGCATGGGATGGCAGAGTTTTTG
GATAAGCATGTGACCTCTGAACAGGAGTGGGACAAGGTTAGTCTCATAAAACAGTGCTCG
TGTGTGATGTATTAGACAGAGCTGGCAGTCCTCATAGTGAAGCTCAGAACAAGAAAAGTT
[G, A]
TCCAGTATTTTTCAGCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCA
TAAACAGTTTATTCCAGAGTTAATCCAAACAGCAGCTATGTAGGATATCAGCCAGGCT
AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG
ATTAACACTACACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCCTATTTTTCATAGGA
ATGGTGTTTGTGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTAT

21477 TCAGCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCATAACAGTTT

FIGURE 2S

ATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCTAGGAGTAGGG
TACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAACCTA
CACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCATTTTTTCATAGGAATGGTGTG
TGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTATTTTAAAGCCA
[G, A]
TCAGATTTAGCAGGCAGAGACATTTTCAGACATCTAAAGTGTTGATGTATTTTCATACCTTT
AACTGTGCTTAAATTAGGATCTCCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGTA
GGTCCAAGGTCTTGGGCCTCTTAATTTTTCAAACCTCAAAACTTGACAGCAGTTATCTTT
GGAACGTGCTGATTTGTGCTTCTTAAGTTAACAGCATACAATGACTGCTAGAAATCAATTT
CTGCATTTAAGGTGAAGTTAGCCGGGTACTATGGTTTACCTGTAATCTCAGCACTTTGGG

22230 GGATTGCTTGAGCCCAAGAGTTGAAGTTGCAGTGAGCCATGATTGTGCCACTGCACTCC
AACGTGGGTGACAGAGCAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAACCTTCT
GGCCAAGAACCAGCACTGGTTATGATAGTAACCTATTTTCTGTTGTGCAGATTTATTCAG
GAACTTAATTTTAGGTTGTTGAATAGAAGTTTGTATCAGATAAAATTGAATTAACAAAA
ATTTTTTTTGAGACAGGGTCTTGCTGTTATCCAGGCTGGTGTGTAGTGGTGTGATCACGG
[C, T]
TCCCCGCAGCCTCAACCTCCTGGGCTCAGGTGATCCTCCACCTCAGCCTACCGAGTAGC
TGTAACCTACAGTGATGACACCATACCAGGCTCATTTTGTACATTTTGTAGAGAGAG
GGTTTTGCCATGTTGCCAGGCTAGTCTCAAACCTCCTGGCATCAAACAGTCCTCCCACTC
TGGCCTCTCAAATGTTGGGATTACAGGCATGACCAGCCAATTATTTCAAGGAGTTATTTT
TTTTCTTCTACTTTGGGGGAAGATGAATTATATAAGTCTCCATTTTAGGAGTATTTCTAC

22941 AATTTCTGTCTACCTAATTTTCAGCAAGATTTCACTCTTTTCATGTTACTTTTGTCCCAGA
ACAAATTTCAAGTGCTTCTCTTACCTGTGCATTTCTCCCCCTGATTAGTCTCTGGCTT
TGTAATTACTTTTCAGTCAGAGACGACTTTTTTTTTTTTGAGACAGGGTCTCACTCTGTCA
CAGACTGGAATGCAGTGGCACAGACAAGGCAGCCTTGACCTTCTGGGCTCAAGCAATCTT
CCTTGCCCTCAGCCTCCTGAGTAACCTGGGACCACAGGCACGTTGCCACCATGCCTGGCTA
[A, G]
TTTATTTTAATTTTTATTATTTTTTGAGACAGGGTATTGCTCTGTCAACCAGGCTGGAGTG
TAGTGGCATGATCAAGGCTCACTGCAGCCTTCACTCCTGTGCTCAAGCAGTCCTCTCAC
CTCAGCCTCCCCATTAGCTGGGACTATAGGTCCACACCACTACACCAGGCTAATTTTGT
AATTTTTTGGTAGAGACAGGGTTTCATCGTGTGCTAGGCTGGTCTTGAGCTCCTGGGC
TCAAGCGATTACCTGCCTTAGCCTCCCAGGTGTGAGCCACTACACTCAGCCTTTTAAAA

23963 ATACTACCTAGTTTTGAACTCTTAGCCCCCTGCCACAGACACGGCAGCCCCCTTGAACCTTC
CTGGGTTCAGCGAGCCTCCTACTTCAGCCCCCTGAGTAACCTGGGACCACTGGCCTGTGT
CACTGTGCCTGGCTAATTTTTTTTTTCTCCTCACATGGGCAATGTTGGGCAAGTTAAATC
GACTTCTTTGTGCCTCAGTTTCCTCATCTGAAATGGAGATCATACTGCTATGTACCTGAT
ACAATGTTTGTGAGGATTGAATGTGCAGAGTTCCTTTTTTCTGTTGTTGTTGTTTGA
[C, T]
GGAGTCTCACTCTG

25686 CTGAAAAATCCTTTAACTCTTGTGGTTGCGGGTGACAGAAAAACAAGCCAGGCCTCCCC
AGGCAGCATAAGGGGATGTGGAAAAATAGGATAGATTGACATGAGTTTGCTTCAGGTAGAC
TGGCTGACTCCCAGGATTACACCCAGTAATCAGTATATTCAAGCCTTGCTGTCTTGAT
TTCTTTTTCAGACGGTCTTTCTCCAAGTGGTGGATATGGTAACAACCCACGTGCACTAGCTT
AACAAAAAGTTCTTAGGAATGGCTTTGTTTCGGCCTGGCGCAGTGGCTCATGCCTGTAATC
[A, C]
CAACAGTTTGAGAGGCCAAGGTGGGCGGATCACCTGAGGCCAGGAGTTTCGAGACCAGCCT
GGCCAACATAGTGAAACCCCGTGTCTACTAAAAATACAAAAATTAGCCGGGCGTGGTGG
CAAGGGCTTGTAATCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG
AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTGCACTCCAGCCTGGGCGACAGAGTG
AGACTCCCTCTCAAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTA

26018 ACCTGAGGCCAGGAGTTTCGAGACCAGCCTGGCCAACATAGTGAAACCCCGTGTCTTACTAA
AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCAGCTACCTGGGAGG
CTGAGGCAGGAGAATCGTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT
GGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC
[A, G]
CCTGGATTACGTCTACACAGTACACACAGAATGGATTTCACCCCAAAGAAAGAAATCTGCG

FIGURE 2T

GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTGT
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTACCTTTT
GCTTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG

26078 AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCCAGCTACCTGGGAGG
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT
GGTTCCTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC
ACCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAGAATTCTGC
[G, A]
GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTGT
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTACCTTTT
GCTTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG
GCTAAGTGTGGTGTCTCATACTTATAATCCCAGTGTCTGAGGCCAGGAGTTCAAGACCAGC

26625 TGTGGTGTCTCATACTTATAATCCCAGTGTCTGAGGCCAGGAGTTCAAGACCAGCCTGAGC
AACACAGCAAGATACCATCTCTATAAAAAATTGTTAGAAAATGATTCTGCTGAAAGAGCA
AAAATAAAAAATTAAAGAAAGTAGAAAAATAAACTAAATTTAAAGATTAACCTGGGCAT
GTTGGCATGCACCTGTATTCTTAGGTATTCTGGGAGGCTAAGGCACAAGGATCCCTTGAGC
GCAGGAGCTCAAGGTTGGATTGAGTTGTAATCACACCACTGCACTCCAGCCTCGTGGCA
[C, G]
AATGAACTGTCTCAAGAAAAAAAAAAGTGACAGAGGGAAACAATATTTGCAATTCATA
GAGCAGATACAGGGTTCATATTCTAATATTAAAAAACTTCTAAAAGTTAAGAAAAAG
GCCAACTGCCCCACAGAAAAATGGGCAAGGAGATAAGAACAGATTGTTACAGGAAGAG
ACACACAGATGATTATTAATAATCTGAAAAAGATGCTGAGTCTTACTCTAAGAAAAATTC
ACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGTAATCTCAACTGCG

27151 TCCTAAGAAAAATTCACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGT
AATCTCAACACTGGGAGACCAAGGCAGGAAGATCACTGAAGCCAGGGTATCGAGACCAGC
CTGGACAACGTAGTGAGACCTTATCTCTTAAACAAAAACAAACAAAAACAAAAA
AACAGTAAAAATTGGCCGGGCACAGTGACTCCTGCCTATAATCCCAGCACTTTGGGAAGC
CCAGGTGAGTGGATCACTTGAGGTGAGGTGTTGAGAACAGCCTGGCCAACATGGCAAAA
[C, T]
TCCGTCTCTACTAAAAATTACAAAAATTAGCCAAGTGTGGTGGCATACTGCTGGTAGGGCA
GCTACTTGGGAGGCTGATGTGAGACTCCATTTAAAAAATAAATCAAAAATTAGCTGGG
TATAGTGGCACACCCCTATAGTCTCGCTCCTTGGGAGGTTGAGGCAGGAGGATTGCCTG
AGCCCAGGAGTTCAAGGCTGCAGTGAACCATGATCACACCACTGCATCTAGCAGCCTGG
GAGACAGAGCAAAACCTTGTCTCAAAACAAACAAACAAACAAAAACAAAAACACTT

28032 AGGAGCAGAGCCCTGCTCTTCTCATTCACTTACTTTATCTGTAAGATAGCATCATTTCTA
CCACACGCTGGTGGTGTGAATAAAATGAGATGAACCTTAGCATAGAGTGCTTAGTAAAG
GTTCTGGACATTTCTAGTAGTGAATCATGCCAAATGTGGTCTAGGTGATTGGCTTCT
TTTGCTAGCATGTTTTAGGGCTCCTCCATGCTGGGGCATTGCATCACTGCTTTATCTCT
TTTTATCGCCTAGTATTATCCACTGTGTGGATAGACCACATTTATCCATTATCAGTTG
[G, A]
AGGATATTTGGGTTCTTCCATTTTTTTTGGCTATGGTGAATAGTACTGTGTACATTTGC
ATATAAGGTTTGTGTAGATGTGTGTTTCTTTTCTTGGGTCTATGCTGAGAAGTGGA
ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGGAGCTGCCAGACGCTTTTCCAAGT
CGCTCCACCATTTTACATTCCCGTCAGCAGTGTGAGAGTCCCAGTTTACCAGCACTTGT
TGTTATCTCTTTTAACTGTATGTATATACTTAACATTTATTTATAATAAATGTACA

28772 AAAATCATCAAGCCGAATCCCACTGTTAGAAATAAAGGTTTTATTTCACTTTCAAGTTA
TCAGGATCCAGGGAGGTGAATACACTTAGAGGATAGACTCAGCTCATTTCCAGCTATG
CCTTTTCAGCAGCATTCTTACCAGAGTAGGAATATAATGTTAGTCATTATTTAGAGGCCTG
GCCATCTTGAGAAGGTTTACTGTTTAGTCTGCAGTACAATTATAACTGTTTTTGTATATT
GGGTATTTTTTTTTCAGAAGTAGGCCAGTAGCTCTAACAGGAGCCTCTTTAGCCTGAATTC
[G, A]
TCCAAGTAGTGCAGTGTGCACTAGTTGTCCCTCGGGACATGCTCCCCAATACGTAACCTC
ACTTCCAGGTTGCAACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCATGGAGCTTA
AAATGAACCTTGATCTTCGTGAAAGATGAGTCTGCAGCTAAGAGACTTTACTGTATATCAT

FIGURE 2U

AGTGTTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTGACGGAGTCTCACTCTTTCACCC
AGGCTGGAGTGCAATGGCGAGATCTGACTCACTGCAACCTCCGCCCCCTAGGTTCAAGC

29572 TCATAGTTCTTATGCACAAAGACCCCTTAAATATTGTTTGTAATCTCCCCTATGCACAC
GCTGACCTGTTCCCTTAATCTTCTTATCTGTCTAGGTTTGGAGCAGGTATGTTAAGAAGTT
AGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAATGAACTTAT
AACCAATGCACTGCACCACATCCAGATGTCATCACCTACCTTTCGAGACTCAGAAACCA
GAGTGTGTTTAACTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATA
[C, T]
GGGGCTAAAGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATA
TGATTCCCTTAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCC
TTTGCTTCCAGCCACCAAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAAC
CTTCTTTCCGGATTTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCA
CAGTTAAGTCAAGGTCTTTGGCTTAGATTTATGGGGAGTGTGGGTAAACCTGGGTGAA

29761 ACTGCACCACATCCAGATGTCATCACCTACCTTTCGAGACTCAGAAACCAGAGTGTGTT
TAACCTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATACGGGGCTAA
AGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATATGATTCTT
TAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCCCTTGCTTC
CAGCCACCAAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAACCTTCTTTC
[C, T]
GGATTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCACAGTTAAGT
CAAGTCTTTTGGCTTAGATTTATGGGGAGTGTGGGTAAACCTGGGTGAAGCTGTTATC
ATTAAAAAGTCTTCATTAAGCACCTAATTACTGCTGTCTCTTTTCTAGACCCGGCATAAA
AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACCTACACTTTTTAGTTG
CCTTTACCAAGTATTGCAGATACTACTGCAAATAAGTGAAGAAAGTAACAGCATTAACT

30732 ATTCTGTGTGTTGTTGAGAAAGGGAGGAGTGGGGAAGGTAAAAATCTTGACATACTTTCT
TCGTGGGTATTTTTCTTGAGCGATTCCATCTTAGTTGATTAGCAGTTAGCAATTGCCCA
TTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACATCATTTCTTCT
TTTTTCCCTCTCTTCTGTGTCTCTAGGTGATGGCCATTGCCACTTTGGCTGCCTGTTA
TAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCCGAAAGGGCAAGCAGTGACCCT
[G, C]
ATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAGTATATGGAAGAG
GTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGATTTAGTAATGTCA
CTGTTTAACCAGGTTTGGATATTAGATGATCCTAAACAATTCATATCCTGTGGCCTAAAG
AGACAGGAATTGATATCCTTTATAAGGAAAAAGTCTATTACAGGAGCCGAGCAGATTG
CTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCTGTAGGTTGGAG

30841 GCAATTGCCCATTTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACA
TCATTTCTTCTTTTTTCCCTCTCTTCTGTGTCTCTAGGTGATGGCCATTGCCACTTTG
GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGAAAGGGCAA
GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG
TATATGGAAGAGGTGGGTTTTATTAACTACTTGGATAATTTGTAGCTACTTTTATGAT
[G, T]
TAGTAATGTCACTGTTTAAACCAGGTTTGGATATTAGATGATCCTAAACAATTCATATCCT
GTGGCTAAAGAGACAGGAATTGATATCCTTTATAAGGAAAAAGTCTATTACAGGAGC
CGAGCAGATTGCTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCT
GTAGGTTGGAGCCCCCTCAGTAGAATCATAGATTTTGAGCTGCAAGATGATGCAGGAGGCC
AACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTGATGCAG

31376 GAGGCCAACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTG
ATGCAGTGCGTGATTGAGTGGATCTCTGGCTCCCGTCCATGTGTCTGACACCCAGTCTG
GTACTTTCATTATGCCACAGGCCTCAATTGAAAAATCACAGTAGGGAATTTAGGCCAAGG
AAAGCCATCAAGTTGCAATTATTTCTAAATTTTCTTTGGAAAAATTCATTTCAAATACC
AAAACCATCCTATAAAAAGAAAACCTTACCTTCTTAGGTCAAATCTCTAATATTTGACTAG
[G, A]
TTCAAAAAGTTTATTTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTTGG
GAGACCAAGGTGGGAGGATCACTTGAGGCCAGGAATTCAGACCAGCCGGGCGACATAG
CAAGACCCCATTTCTACAAAAAATTTAAAAATTTGTCATGGTGGTGCACGCCTGTGGTCCC
AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTCGAGGCTACAGTA
AGCTGTGTGATTTTCATTCATTCGACTCTAGCCTGGGTGATAGAGTGAGACTTTGTCTCAA

FIGURE 2V

32032 TCTCTAGGCCCTAGAGCAGTGGTTTGTAAATGGAGGTGATTTGCTCCCCTCCCCCAGAG
GACATTGGACAATGTCTGGAGACATTTTGGATTGTCTAACCAGGCAGGAATCGGGTGCTA
CTGGCATCTGGTGTAGTAGAGGCCAGGATGATGCTGTGATCCTCAGGTGTGATCCTGTTG
AGAATGAAACACTGTAGACTTTATGAAAACATACAAGACCCTCATCATTTTCCCTTGCC
TGAGCTCCCTCCCAGAGGTTACCTCTGTTTCATGGTTTGTGCATCCGTCTAGTCCCCT
[A, G]
TTACGCGTTTACAGGAATATGGTTTGCACAGTGTTCATCTAAATAGAATTATACAAA
ATAGCGATTTCTGATTTCTCTTGCAATTTGCACATTCTTCTTATACTTCTCCCTACCTT
TATCTGACACAGAAATGCTGTATGTCCAGAACTTCTATCAGAGGCACCTATGGAAGTCTA
AGGGAAGACCACATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATT
CAGCCAGTGACCCAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAA

32525 ATCGCTTTTAAAAACCTAAAATTTTGTAGTCACTAGATGAAAATATTAGCCAGTGACC
CAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAACTTACTTTGATC
TATGTGCTGGGGTAGTGACCAAGTAGGTGGGTAGGAGTAATCTCAGGGAACTTGAGGC
CCCAGCCTCATGGCTAGGGTCATAATTTGAACCCAGGTCTGTCTGACATCAGAAATCCATG
ATGTTAACCCCAATTCTAAGGGGTTCAACTACCCTTTCTAAATGGAATCCTGCTATATTA
[A, G]
GCACTATTTATTCAATTTATATAAACTAGAAACATTTTATGTAGTAAGTAGTTGAGAGTG
TTTTGGTTTTGCAGTTTGATCACTAGTTTTAGAAACAGTTTTTAAACACTTTGTGGCCA
ATTCCATTACTATATTAATTTAGATTTATTTGGTTTTTCTTAACTATTGGGATTAAA
TCCTGTTGTAAATTCATAGTTTGAAGGCGAGGGTGGCAGTCTACATTTGGCTGAGCCCT
GTTTTGTGAATAAATGTTATCAGAACACAGCCACACCCATTTGCTTCTATGTCTTCTGT

34179 CTGCTGTATGTAGCACAGCATTGCACAAGAGCTTATTTAGTCTAGTAAACATTTATAGG
AGCCTGTGTCAATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAACT
TTGGGAGGCTGAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAAT
ATGGCAAAACCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACT
TGTCATCCAGCTATTCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAG
[G, T]
TTGTAGTGAGCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTT
TCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGAAAAGTCCG
CTATGACCTGTCTTGCACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGGTTTTAAG
ACCTGAATAATTGAGTTTGAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGG
TTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGT

34249 ATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAACTTTGGGAGGCT
GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAATATGGCAAAAC
CCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACTTGTCTATCCCA
GCTATTCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAGGTTGTAGTGA
GCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACT
[T, C]
CTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGAAAAGTCCGCTATGACCTG
TCCTTGACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAA
TTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTTGGTCTAG
CAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGT
CTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGA

34451 GAGCATCGCTTGAACCTCGGGAGGTGGAGGTTGTAGTGAGCTGAGATGGCACCCTGCACT
CCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACT
TTATGCCGGGCATGTAGATGAAAAGTCCGGCTATGACCTGTCTTGACAAGCAGATGTAAC
TCCTTGATTGAGGCTAGTAGGTTTTTAAAGACCTGAATAATTGAGTTTGAGAAACCTACT
GTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTTGGTCTAGCAACGAAGCATCTAGAAGGTC
[T, C]
CTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCT
CTTCCAGTTGTGCTGTCTGTTTATATGTTAGAAATGATCATCAAGGACTCAAAGTTT
TGCCACTAATTGTATTACCGGGGACTGTCAACCAAGATTTCTCTAATTTATTCACCT
TACTTATCTCCTGGAAGGCATATTGAAGTGCTCTTGGAGTTCTTAAAGGGTTTTGT
TGGTTGTGTATATTCACTTGGGTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCC

34532 AGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGA

FIGURE 2W

AAAGTCGGCTATGACCTGTCTTGACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGG
TTTTTAAGACCTGAATAATTGAGTTTGCAGAACTACTGTGTGCCTTCAGGTAAATGGA
GAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGTCTCTTTGGCCTTACCGGCTCTG
TTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCGACTCTTCCAGTTGTGCTGTCATG
[T, C]
TTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTTGGCCACTAATTGTATTACCGG
GGACTGTCACAACCAAGATTTCTCTTAATTTATTCACCTTACTTATCTCCTGGAAGGGCA
TATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTTGTTGGTTGTGTATATTCACTTGG
GTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCCCAAAGGATGTAAGATGGCTT
ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAAGTAAATGAAGAAA

36541 GGTAGGAGCCAGTTGAAGGGACGTGGGAGGCGCATTCAGAGAGAAGGAGTGGTATGAGA
CTGGAACAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTT
TGTTTTTGTGTTTTTTTGGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGG
CATGATCTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCACCCCAGT
CCCCAAGTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATT
[T, C]
TGTAGAAAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAG
TCTACATGCCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCA
CGGCAACTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGG
TGCAGTAGGTCTGGACCATGGGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTT
TCTCCAGGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGG

36607 CAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTTTGTGTTT
TGTTTGTGTTTTTGGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGAT
CTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCACCCCAGTCCCCAA
GTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTGTAG
AAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTAC
[A, G]
TGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCA
CTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGT
AGGTCTGGACCATGGGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTTCTCCA
GGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAG
TGTAGAGCAGACAGGTAGATTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATA

36681 GACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGATCTCGGATCACTGCA
ACCTCCACCTCCAGGCTCAAGTGATCTTCCACCCCAGTCCCCAAGTAGCTGGGGGACC
ACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTGTAGAAACAGGGTTTTAC
TGTTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTACATGCCTCAGCCTCC
TGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCAACTGTTACTAGACT
[A, G]
TAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGTAGGTCTGGACCATG
GGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTTCTCCAGGTGAGAGGGCTGG
TGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAGTGTAGAGCAGACAG
GTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG
CACTCAGGCGCTAATCTCAGGCAGTAATTTAGGGATGTAGGGGAAGAGATGGATTCTGC

37493 TGACGTTTATTGGGCCTGGCACTGTGAGGTGCTGGGGATGTGAAGATCATTGTGGCTCAG
CCGCTGCTCTCGAGGGCTCTGGGTGCAGTATGCACACCTGTGCCTCCTGTTTGCTCAGG
AAGACAGGCTTTGAGATGAGCTGGGGCTGACATCCCCACCTTATCATTTGGGATGGCTTG
GGTAAGTTATGTTTATGTTCTCTGAGCCTCCCTTTCTCATTGGTAAAATGGGTATAAAA
TACCTGCCAGTGAGGGTTGTTGTAAGTAGCCATGGAAAATGTAAAGCACATAGCACTTA
[C, T]
CATTTTTTCTGTGTCTTTAAACAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCT
AGCAAAACAAGGCAGATCATCTCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTG
ATTTCCCGAAGCCACTACTCCCCCATCTACCTGTCTGTTGTGTCATGCTTTTGGCTGCCTG
AGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCAGACTGGAGAA
CACTGATCCCAAATTTGTCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTCT

37966 CTGCCCTGAGCTGGCAGTACCTGACCACCTCTCTCCAGGTAACAGAAGACTATGTTTCAGA
CTGGAGAACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACT
TTTTTTCTTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCT

FIGURE 2X

AAAAGAACGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAA
ACATGAAAAGGAAAGGGTGCCTCATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTG
[C, A]
TGCTTGTGGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGT
GACTGTGATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAA
TTTGAAGCACCATTGTAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTC
GGCTCCTATTTTTCTCATCATTTTGTTCCTTAATTGGGTTGAATGGAGTAGATAGAAA
TATTTATGGTTTAGGTAACAGTTAGATGTTTCTTAAGAATGCAAACTGCCTTTTCCACAC

37973 GAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTTCAGACTGGAGA
ACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACTTTTTTTC
TTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTTACTACTTTAATCCCTAAAAGAA
CGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAA
AGGAAAGGGTGCCTCATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTG
[T, C]
GGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTC
ATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAG
CACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTCCGGCTCCT
ATTTTTCTCATCATTTTGTTCCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTAT
GGTTTAGGTAACAGTTAGATGTTTCTTAAGAATGCAAACTGCCTTTTCCACACAAAGGCT

38113 TCTCTTTATTTTTTCTTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTT
TAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCC
AGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGAGCATT
AGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTAT
GATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTA
[C, A]
TAGTAGAAAATGATGTGAATTTTCTTCTGTTCCGGCTCCTATTTTTCTCATCATTTTGT
TTCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGAT
GTTTCTTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATCTGGGTAT
TCTCGTATTCTCATTTAAAGGAGTTTAGCTTTTCTAGAGAGAAACAGCAGGATTGCTTTTGA
CCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAGAA

38298 CACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTATGATCC
TGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTGTAATGTTTCGTACTAGT
AGAAAATGATGTGAATTTCTTTCTGTTCCGGCTCCTATTTTTCTCATCATTTTGTTCCT
TTAATTGGGTTGAATGGAGTAGATAGAAAATATTTATGGTTTAGGTAACAGTTAGATGTTT
CCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATCTGGGTATTCTC
[G, C]
TATTCTCATTTAAAGGAGTTTAGCTTTTCTAGAGAGAAACAGCAGGATTGCTTTTGACCTTT
TAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAATTTAA
TTGCTCTGCATTTGTCAAGTACAGTTTCGCTTGAAAGCCTGCCTGACTGTGGAAAAGATGG
AGCTCAAGAATGGAGTTGATGGCCAGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTT
GGGAGGCTGAGGCGGTTCGGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG

FIGURE 2Y